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ALIGNMENTS

| | CDS | gene | | source | FEATURES | · | TITLE | AUTHORS | REFERENCE | PUBMED | JOURNAL | TITLE | AUTHORS | REFERENCE | | ORGANISM | SOURCE | KEYWORDS | ACCESSION | | DEFINITION | RESULT 1 AJ583159 |
|---|---|--------|---|--------|---------------------|---|-------|---------|--------------------|--------|---|---|--|--|--|------------------------|--------|---------------------------------------|-----------|------|---|----------------------|
| /gene="alx1" /gene="alx1" /codon_start=1 /product="NADH L-xylulose reductase" /protein_id="CAB47547.1" /protein_id="CAB47547.1" /db_xref="GI-142820318" /translation="MTDYIPTFFPDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDI /ctranslation="MTDYIPTFFPDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDI /boektraakgaeyhkyateelkkevpkwgsyaCD15DSDTVHKVFAQVAkDFGKLPLH DOEKTAAKQAEYHKYATEELKLKEVPKWGSYACD15DSDTVHKVFAQVAKDFGKLPLH SUNTAGYCENFPCEDYPAKNAEKWVKVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGS MSGAIVNDQNQVVYNMSKAGVIHLAKTLACEWAKKYNIRVSLNGGYYGPLTKNVIN GNEELYNRWISGIPQQRMSEPKEYIGAVLYLLSESAASYTTGASLLVDGGFTSW" | Years = 'alx1' 1. 816 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. | 1. 816 | /organism="Ambrosiozyma monospora" /mal_type="mRNA" /strain="NRRL Y-1484" /db xref="taxon:43982" | 1816 | Location/Qualifiers | 1500, Tietotie 2, Espoo, 02044 VTT. FINLAND | | • | 2 (bases 1 to 816) | • | Catabolic Pathway of Yeast J. Biol. Chem. 279 (15), 14746-14751 (2004) | A Novel NADH-linked L-Xylulose Reductase in the L-Arabinose | Verho, R., Putkonen, M., Londesborough, J., Penttila, M. and Richard, P. | Saccharomycetales; Saccharomycopsidaceae; Ambrosiozyma. 1 | Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; | Ambrosiozyma monospora | | alx1 gene: NADH L-xvlulose reductase. | | ne). | Ambrosiozyma monospora partial mRNA for NADH L-xylulose reductase | |

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Query Match
Best Local Similarity
Matches 528; Conserv
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1 (bases 1 to 1166)

Maray, J.S., Wong, M.L., Miyada, C.G., Switchenko, A.C., Goodman, T.
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Direct Submission
Submitted (10-AUG-1993)
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Isolation, characterization and expression of the D-arabinitoal dehydrogenase in Candida tropicalis Gene 155 (1), 123-128 (1995)
                                                                                                                                                                                                                                                               Cincinnati College of Medicine, 45267-0560, USA
                                                                                                                                                                                                        ACCAAGAAAAGACTGCTGCCAAACAAGCCGAATACCACAAATACGCTACTGAAGAATTGA
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                                                              CTGATACCGTTCACAAGGTGTTTGCTCAAGTTGCTAAGGATTTTGGTAAGTTGCCATTGC
                                                                                                        AAGGAAAACACGAATCTCCAATTGGTCAAGTCAGTGCTTGGTCCTGTAACATTGGTGATG
                                                                                                                                          AGTTGAAAGA------AGTTCCAAAGATGGGTTCATATGCCTGTGATATTTCTGATT
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/clone="pCT1A"
/clone_lib="genomic_DNJ
and_J.C._Loper"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=experimental
/product="b-arabinitol dehydrogenase"
/protein_id="AAA66355.1"
/protein_id="AAA66355.1"
/db_xref="GI:392786"
/translation="MDSSSYMSYDNIVPSFRLDGKLVIITGGSGGLSAVVSRALLAKG
/translation="MDSSSYMSYDNIVPSFRLDGKLVIITGGSGGLSAVVSRALLAKG
ADIALIDMNLERTQQAAENFPAESYMSKAGKIHSPIGOVSAMSCNIGDAEAVELTFKA
INEHHGKVASVLINTAGYAENFPAESYPAKUAENIMKYNGLGSFYVSQAFARFLIQNN
MTGSIILIGSMSGTIVNDDQPQCMYNMSKAGVIHLARSLACEMAKYNIRVNTLSPGYI
LTPLTENVISGHTEMKTEMESKIPMKRMAEPKEFVGSILYLASDSASSYTTGHNLVVD
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/mol_type="genomic DNA'
/strain="ATCC 750"
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Pred. No. 1.7e-73;
0; Mismatches 272
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Candida
                                                                                                                                                     Direct Submission
Submitted (18-MaX-1993) Brian Wong, Department
Medicine, University of Cincinnati College of P
                                                                                                                                                                                                                                                                                                                                                                                                                                biosynthetic pathway and the gene that encodes NAD-dependent D-arabitol dehydrogenase

J. Bacteriol. 175 (19), 6314-6320 (1993)
                                                                                                                                                                                                                                                                                                        Wong, B., Leeson, S., Grindle, S., Magee, B., Brooks, E. and D-arabitol metabolism in Candida albicans: construction analysis of mutants lacking D-arabitol dehydrogenase J. Bacteriol. 177 (11), 2971-2976 (1995)
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1 (bases 1 to 1614)
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Candida albicans
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  /organism="Candida albicans"
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  AAATGAAGACAGAATGGGAATCAAAGATCCCAATGAAGAGAATGGCAGAACCAAAAGAGT
                               AATTGTACAACAGATGGATCTCTGGTATCCCACAACAAGAATGTCCCGAACCAAAGGAAT 724
                                                                                                     CTTTAAACCCAGGTTACATCTACGGTCCTTTGACCAAGAATGTTATCAATGGTAACGAAG
                                                                                                                                                                                                                                                                       CTGGTGCCATTGTCAACGATCCTCAAAACCAAGTTGTCTACAACATGTCCAAGGCTGGTG
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                                                                               CATTGTCGCCAGGGT
                                                                                                                                                           TCATTCATTTAGCCAGATCATTGGCCTGTGAATGGGCTAAATACAATATCAGAGTCAACA
                                                                                                                                                                                                 TTATCCATTTGGCTAAGACTTTGGCTTGTGAATGGGCTAAGTACAACATCAGAGTTAATT
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/transl_table=12
/product="p-arabinitol dehydrogenase"
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/product="p-arabinitol dehydrogenase"
/db_xref="GI:295568"
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/translation="MDSAYMSYDNIVPSFRLDGKLVILTGGSGGGLAAVVSRALLAKGA
/translation="MDSAYMSYDNIVPSFRLDGKLVILTGGSGGLAAVVSRALLAKGA
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Pred. No. 1.3e-
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                                                                                     CTGGTGCCATTGTCAACGATCCTCAAAACCAAGTTGTCTACAACATGTCCAAGGCTGGTG
                                                                                                                                                                                                 ACGCTGAGAAGATGGTGAAGGTTAACTTGTTGGGTTCTTTGTATGTTTCTCAAGCCTTTG
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                            TTATCCATTTGGCTAAGACTTTGGCTTGTGAATGGGCTAAGTACAACATCAGAGTTAATT
                                                                                                                   CCCGTCCATTGATCA----GCAGCAATAAGAAAGGATCCATCATTTTAGTTGGGTCGATGT
                                                                                                                                               CTAAGCCATTGATCAAAGAAGGTATCAAGGGTGCTTCTGTTTTTGATTGGTTCTATGT
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Saccharomycetales; Saccharomycetaee; Pichia.
1 (Dases 1 to 1157)
Hallborn,J., Walfridsson,M., Penttila,M., Keranen,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (30-NOV-1994) Johan Hallborn,
Institute of Technology, Chemical cente
S-221 00, Sweden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A short-chain dehydrogenase gene from Pichia stipitis having D-arabinitol dehydrogenase activity
Yeast 11 (9), 839-847 (1995)
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P.stipitis ARDH gene
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/evidence=experimental
/product="D-arabitol dehydrogenase"
/product="D-arabitol dehydrogenase"
/protein_id="CAA86939.1"
/db xref="GI:763164"
/db xref="GI:763164"
/db xref="Uniprot/Swiss-Prot:P50167"
/db xref="Uniprot/Swiss-Prot:P5016
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191. .1027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Pichia stipitis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        function="NAD dependent,
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er, Getingevagen 60, Lund,
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Query Match Best Local Similarity

32.9%;

Score 268.4; DB 8 Pred. No. 3.6e-57; 0; Mismatches 311

DB 8;

Length

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Sequence 6 :
AR031556
AR031556.1
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1 (bases 1 to 696)
Hallborn,J., Penttila,M., Ojamo,H., Walfi
Keranen,S. and Hahn-Hagerdal,B.
Xylose utilization by recombinant yeasts
Patent: US 5866382-A 6 02-FEB-1999;
Location/Qualifiers
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                                                                     Unclassified.
                                                                                            Unknown
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                                                                           TITLE
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Hallborn, J., Penttila, M., Ojamo, H., Keranen, S. and Hahn-Hagerdal, B. Production of ethanol from xylose Patent: US 6582944-A 6 24-JUN-2003, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTACACTACGGGCCACAATTTGGTTGGTGGACGGAGGAT
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/organism="unknown"
/mol_type="unassigned
/organism="unknown"
/mol_type="mRNA"
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Pred. No. 1.7e-49;
0; Mismatches 203
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Sequence
AR544898
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Patent: US 6747137-A 29 08-JUN-2004;
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Weinstock, K.G. and Bush, D.
                                                                                                                                                                                                                                                                                                                                                                                                     Unknown
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 CTGAAGCTTTAATCAAGGGTTTGTTGGCCTACGGTTCTGACATTGCTTTGCTTGATATCG
                                       TCCCAAGCTTCCGTTTGGATGGAAAACTAGTCATATTAACCGGTGGCTCTGGTGGTTTGG
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/mol_type="genomic
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Pred. No. 1.5e-44;
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Best Local Sim
Matches 287;
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Fragment Name CR382133_00 CR382133_01 CR382133_02
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Local Similarity 56.3%;
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Candida albicans

Candida albicans

SM Candida albicans

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

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Sou2p

4293 bp (SOU2),

s bp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-MAY-1997) Department of Biochemistry and Biophysics, University of Rochester, 601 Elmwood avenue P.O. Box 712,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Janbon, G., Rustchenko, E. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Rochester, NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Janbon, G.,
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                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SOU1"
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KKNKSGSLIITSSMSGTIVNIFQLQAPYNAAKAACTHLAKSLSVEWASFGARVNSISP
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/transI_table=12
                                                                                                                                                                                                                                                                                                                   note="Vacuolar H+-ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="short-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="SOU2"
356. .1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mol_type="genomic DNA"
strain="Sor17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="SOU2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome="4"
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                                          10.7%;
49.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      TDIADFADPEMKKKWWQLTPLGREGLPQELVGAYLYLASNASTYTTGSNIAVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  xref="taxon:5476"
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14642, USA
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                          <u>.</u>
                      Score 87.2; DB 8;
Pred. No. 2.9e-11;
0; Mismatches 303
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    Submitted (20-MAR-2004) Center for
                                        Dean,
                                                      Laboratory, North carolina State
Raleigh, NC 27606, USA
3 (Dases 1 to 126105)
Thon, M.R., Mitchell, T., Brown, D.E
                                                                                                                                     Submitted (05-JAN-2002) Plant Pathology -
                                                                                                                                                           Direct Submission
                                                                                                                                                                           Dean,
                                                                                                                                                                                                                                                                      Sordariomycetes incertae sedis; Magi
1 (bases 1 to 126105)
Thon, M.R., Mitchell, T., Brown, D.E.,
                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE2.
Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Magnaporthe grisea chromosome PROGRESS ***, 2 ordered pieces
                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                    The sequence of Magnaporthe
                                                                                                                                                                                                                                                          Dean, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTCTTTAAACCCAGGTTACATCTACGGTCCTTTGACCAAGAATGTTATCAATGGTAACG 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGTTATCCATTTGGCTAAGACTTTGGCTTGTGAATGGGCTAAGTACAACATCAGAGTTA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 126105)
an,R.A. Dr, Mitchell,T.
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                        Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126105 bp
                                                          Brown, D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  pieces
                                                                                                                                                                           Dr,
                                                                                                                                                                                                                                    grisea
                                                                                                                                                                           Thon, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone 18L14,
                                                                                                                 University,
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Integrated Fungal Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2902
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                                                          Diener,
                                                                                                                                                                                                                                                                        Diener, S.,
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2702

2642 541 2582 481 2522 421

2813

2753

and Fungal

Brown, D

Taro, A.,

Pan, H.

and

840

Main Campus Drive,

Genomics

linear

HTG 20-MAR-2004

SEQUENCING

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Taro, A.,

Pan, H.

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Best Local S
Matches 181
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On Mar 20, 2004 this sequence version replaced gi:18071329.
On Mar 20, 2004 this sequence version replaced gi:18071329.
NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
are represented as runs of N. The order of the pieces
to the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 1 86195: contig of 86195 bp in length
86196 86395: gap of unknown length
86196 126105: contig of 39710 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56380
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Sequence
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                                                                                                                                                                            Patent: US 6747137-A 2490 08-JUN-2004;
                                                                                                                                                                                                         1 (bases 1 to 927)
Weinstock,K.G. and Bush,D.
Nucleic acid sequences relating to Candida albicans for diagnostics and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown
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/mol_type="genomic DNA"
/db_xref="taxon:148305"
/chromosomee="7"
/clone="18L14"
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                         GTGCCAGCTTACTGGTTGATGGTGGTTTCAC 809
                                                                               AGGAATACATTGGTGCTGTTTTGTACTTGCTTTCTGAATCTGCTGCTTCATACACTACTG 778
                                                                                                                           ATCCGGATGTCAAGAGTAAATGGTTGCAACTTACACCACTTGGTAGAGAAGCCAAACCAA
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Search completed: July 12, Job time: 3865 secs 2005, 13:24:19

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     nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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geneseqn2003ds:*
geneseqn2004as:*
geneseqn2004bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length DB
     816
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687
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1186
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8798
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                                                                                                                                                                                                                             ADS61049
ADS48561
AAH74598
AAF12302
ADS47380
ADS47380
ADS48180
AAF11343
                                                                                                                                                   AAL57425
AAZ46762
AAZ46763
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                                                    ABZ13143
                                                                                                                              AAC42189
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                  Ad847380 Bacterial
Adno2512 A. thalia
Ads48180 Bacterial
Aaf11343 Aspergiil
Aa157425 Datura st
Aa246762 Bacillus
Aa246763 Bacillus
Aa24763 Bacillus
Aa24763 Arabidops
Aa157426 Hyoscyamu
Aac43167 Arabidops
Ab213143 Arabidops
Ab213143 Arabidops
Ab132514 A. thalia
                                                                                                                                                                                                                                                                                                                            Aah74598 Synthetic
Aaf12302 Aspergill
                                                                                                                                                                                                                                                                                                                                                                                                                              Adq94601 Ambrosioz
Aaf07518 Fusarium
Aaf12409 Aspergill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                 Ads61049 Bacterial
Ads48561 Bacterial
Bacteria.
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | c 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 51.2 | 51.2 | 51.2 | 51.4 | 51.6 | 51.6 | 51.6 | 52.2 | 52.4 | 52.4 | 52.8 | 52.8 | 53 | 53 | 53.2 | 53.2 | 53.2 | 53.2 | 53.8 | 53.8 | 54.4 | 54.4 | 55 | 55.2 | 55.2 |
| 6.3 | 6.3 | 6.3 | 6.3 | 6.3 | 6.3 | 6.3 | 6.4 | 6.4 | 6.4 | 6.5 | 6.5 | 6.5 | 6.5 | 6.5 | 6.5 | 6.5 | 6.5 | 6.6 | 6.6 | 6.7 | 6.7 | 6.7 | 6.8 | 6.8 |
| 810 | 810 | 711 | 849 | 855 | 852 | 852 | 852 | 789 | 656 | 1366 | 819 | 774 | 774 | 855 | 855 | 852 | 852 | 1003 | 768 | 783 | 783 | 949 | 943 | 732 |
| œ | δ | 11 | თ | 12 | 12 | 12 | 12 | 12 | σ | 12 | 11 | 13 | σ | 12 | 12 | 12 | 12 | 12 | 13 | σ | w | 6 | 12 | 13 |
| ABZ42061 | ABZ13885 | ADJ12134 | ABZ32459 | ADJ98101 | ADJ98113 | ADJ98115 | ADJ98109 | ADN62500 | ABQ65920 | ADN62538 | ADJ12063 | ADS01477 | ABN91262 | ADJ98105 | ADJ98103 | ADJ98097 | ADJ98111 | ADN62520 | ADS48201 | ABZ13220 | AAC43166 | ABN98571 | ADN62526 | ADS63285 |
| Abz42061 Arabidops | Abz13885 Arabidops | Adj12134 Maize CDN | Abz32459 Candida a | Adj98101 Ketoreduc | Adj98113 Ketoreduc | Adj98115 Ketoreduc | Adj98109 Ketoreduc | Adn62500 A. thalia | Abq65920 Arabidops | Adn62538 A. thalia | Adj12063 Maize cDN | Ads01477 Staphyloc | Abn91262 Staphyloc | Adj98105 Ketoreduc | Adj98103 Ketoreduc | Adj98097 Ketoreduc | Adj98111 Ketoreduc | Adn62520 A. thalia | Ads48201 Bacterial | Abz13220 Arabidops | Aac43166 Arabidops | Abn98571 Arabidops | Adn62526 A. thalia | Ads63285 Bacterial |

ALIGNMENTS

RESULT 1
ADQ94601
ID ADQ9

ADQ94601 standard; cDNA; 816

BP.

ADQ94601;

23-SEP-2004

(first entry)

Ambrosiozyma monospora NADH dependent L-xylulose reductase cDNA.

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WPI; 2004-517001/49.
P-PSDB; ADQ94602.
                                                                     16-FEB-2001; 2001FI-00000308.
15-FEB-2002; 2002WO-FI000155.
10-WAR-2003; 2003FI-00001307.
                                       Verho R,
                                                                                                              24-NOV-2003; 2003US-00720018.
                                                                                                                              08-JUL-2004.
                                                                                                                                              US2004132074-A1.
                                                                                                                                                                                                                                     Ambrosiozyma monospora.
                                                                                                                                                                                                                                                             NADH dependent L-xylulose reductase; fermentation; biomass; ALX1; gene;
                                                     (VALW ) VALTION TEKNILLINEN TUTKIMUSKESKUS.
                                      Richard P,
                                                                                                                                                                                     /product= "Ambrosiozyma monospora NADH dependent
xylulose reductase"
                                                                                                                                                            /partial
/note= "No stop codon"
/EC_number= "EC 1.1.1.10"
                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                      *tag= a
                                       Penttila
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New DNA molecule encoding NADH dependent L-xylulose reductase, useful in

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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      816 BP; 217 A; 159 C; 182 G; 258 T; 0 U; 0 Other;
                                                                                           GAATACATTGGTGCTGTTTTGTACTTGCTTTCTGAATCTGCTGCTTCATACACTACTGGT
                                                                                                                                          GAAGAATTGTACAACAGATGGATCTCTGGTATCCCACAACAAAGAATGTCCGAACCAAAG
                                                                                                                                                                                                                                                                                                         GGTGTTATCCATTTGGCTAAGACTTTGGCTTGTGAATGGGCTAAGTACAACATCAGAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTGGTGGTTTAGCTGAAGCTTTAATCAAGGGTTTGTTGGCCTACGGTTCTGACATTGCT
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                                                                                                                                                                                                                                                 AATTCTTTAAACCCAGGTTACATCTACGGTCCTTTGACCAAGAATGTTATCAATGGTAAC
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                        GCCAGCTTACTGGTTGATGGTGGTTTCACTTCTTGG 816
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Pred. No. 2.
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1.7e-227;
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308 TGGTTAACACAGCTGGTTACTGTGAAAACTTCCCATGTGAAGATTACCCAGCCAAGAACG

Query Match Best Local S Matches 265

Similarity

12.2%;

Conservative

<u>.</u>

Score 99.4; DB pred. No. 4.5e-1 0; Mismatches 2

; DB 3; 1.5e-18;

231; Indels

7;

Gaps

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The present invention describes a method for monitoring differential CC expression of genes in a first filamentous fungal (FF) cell relative to CC expression of the same genes in one or more second filamentous fungal CC cells. The method uses fluorescence-labeled nucleic acids isolated from CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs care used in the methods for monitoring differential expression of genes CC in a first filamentous fungal (FF) cell relative to expression of genes CC in a first filamentous fungal (FF) cell relative to expression of the methods for monitoring differential expression of the microorganisms to be improved. New genes may be discovered, CC global expression of genes from FF cells allows the production potential CC of the microorganisms to be improved. New genes may be discovered, CC possible functions of unknown open reading frames can be identified and GC gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture CC conditions, environmental stress, spore morphogenesis, recombination, CC metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random CDNA clones including elimination of CC redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 CC represents ESTs from Nepergillus niger; AAF11854 to AAF11853 represents ESTs from CC ESTs from Aspergillus niger; AAF11879 to AAF11878 represents ESTs from CC invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombina culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monitoring differential expression of genes in filamentous fungal uses fluorescence-labeled nucleic acids isolated from the cells are substrate of expressed sequence tags.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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 Sequence
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ID AAF12409
ID AAF1
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XX Mult
KW AASPE
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Claim 88; Page 2078; 3161pp; English
                                                                                           Monitoring differential expression of genes in filamentous fungal uses fluorescence-labeled nucleic acids isolated from the cells ar
                                                                                                                                                                                                    WPI; 2000-594572/56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multiple gene expression; filamentous fungal cell; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus oryzae EST
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                                                                of expressed sequence tags.
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cc same genes in one or more second filamentous fungal cells. Monitoring the close spread on the expression of genes from FF cells allows the production potential cof the microorganisms to be improved. New genes may be discovered, cc possible functions of unknown open reading frames can be identified and cells conditions, environmental stress, spore morphogenesis, recombination, cc metabolic or catabolic pathway engineering. Using ESTs provides several cadvantages over genomic or random cDNA clones including elimination of cellular cells advantages over genomic or random cDNA clones including elimination of cellular cells 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the
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Query Match Best Local Sim Matches 279; Sequence Similarity 687 Conservative BP; 152 A; 210 10.9%; Score 88.6; DE Pred. No. 3.3e-0; Mismatches C; 175 G; 147 6; DB 3; 3.3e-15; T; 0 U; 3 Other; Length 687 6 Gaps

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GTTACCTTTCTGCTCAGNGA 667
                                                                                                                                                                                                                                                                                           GGTTACATCTACGGTCCTTTGACCAAGAATGTTATCAATGGTAACGAAGAATTGTACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACAACGTGCCGCAGCCCCAGGCTCCTTACAACGCCGCCAAGGCCCGCTGTTCGTCAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTGGGGCGTTAATGTCGATGGAACATACCTTTTCGCCACCGGTGTCGCCAAGC---AC 347
                                                                                                                AAGTGGATCTCGCTCATCCCCACCGGCAAGATGGGTACTCCCGAGGACCTGATGGGTCCC
                                                                                                                                                                                                                                   CGATACATGCTTACTGCCCTGACCCGCAAGATTTTGGATGAGAACCCCCGATTGCGGGAC
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                                                        GTTTTGTACTTGCTTTCTGA
                                                                                                                                                                        AGATGGATCTCTGGTATCCCACAACAAAGAATGTCCGAACCAAAGGAATACATTGGTGCT 735
                                                                                                                                                                                                                                                                                                                                                         GCCGCGTACTTCGCCGGCGAATGGGCCCGGTCACGACATCCGGGTGAGCTGCATGAGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                 GCTAAGACTTTGGCTTGAATGGGCTAAGTACAACATCAGAGTTAATTCTTTAAACCCA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGGTGAAGGTTAACTTGTTGGGTTCTTTGTATGTTTCTCAAGCCTTTGCTAAGCCATTG 435
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CC microbial source: The invention also relates to a transformed plant CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC having an improved property comprises transforming a plant with the CC recombinant DNA construct and growing the transformed plant, where the CC polynucleotide or polypeptide is useful for improving plant with the CC improved plant properties, e.g. improved cold, heat or drought tolerance, CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests, CC increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of CC content, improved yield by modification of carbohydrate, nitrogen or CC content, improved yield by modification of carbohydrate, nitrogen or CC condition, improved lignin production or improved galactomannan CC providing improved lignin production or improved galactomannan CC production. This sequence represents a bacterial polymucleotide used in the scope of the invention. Note: The sequence data for this patent did cc not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathogen tolerance; pest tolerance; plant disease resistance;
cell cycle pathway modification; plant growth regulator;
homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacterial polynucleotide #13036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADS61049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADS61049 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned in provide for expression of a polynucleotide encoding a polyneptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HINK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CAOY/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mbinant DNA construct; transformed plant; improved plant property; tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAO Y.
HINKLE G J
SLATER S C
CHEN X.
GOLDMAN B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 36723; 122pp; English.
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polynucleotide; gene; ss.
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 T; 0 U; 0 Other;
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Query Match Best Local Similarity

55 . 04;

Score Pred.

81.8; DB 13; No. 3.1e-13;

Length 637;

The invention relates to a recombinant promoter functional in a plant cell, w

nt DNA where

the promoter is positioned

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Claim

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SEQ ID

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26991; 122pp; English.

Sequence 637

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ADS4957 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polynucleotide; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS48561
                                                                                                                        for expression microbial source
                                                                                                                                                                                                                                                                                                                                                   (HINK/)
(SLAT/)
(CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacterial polynucleotide #3304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-DEC-2004
                                                                                                                      New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                              Cao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2003;
                                                                                                                                                                                                                          WPI; 2004-061375/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                                                                                               (GOLD/)
                                                                                                                                                                                                                                                                                                                                                                                                                              CAOY/)
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SLATER
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                              CAO Y.
                                                                                                                                                                                                                                                                                Hinkle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCTCGTCACGTCTGCGGGATTTACCGAAAACTTCGACGCCATCAGCTACCCATACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGGTGCCATTGTCAACGATCCTCAAAACCAAGTTGTCTACAACATGTCCAAGGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
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                                                                                                                                                                                                                                                                                Slater
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                                                                                                                                                                                                                                                                                Chen
                                                                                                                                                                                                                                                                                   Goldman
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RESULT 6
AAH74598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC improved properties, e.g. improved conditions, pathogens or pests, content, improved yield by modification of carbohydrate, nitrogen or conditions, pathogens or plant did and/or construct and growing the transformed plant, where the polymucleotide or polypeptide is useful for improving plant properties. CC improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by condition, improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan cc production. Note sequence represents a bacterial polynucleotide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
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                                                     31-JAN-2000;
08-DEC-2000;
                                                                                                                                              31-JAN-2001;
                                                                                                                                                                                                                                                                      WO200155342-A2
                                                                                                                                                                                                                                                                                                                            Candida magnoliae.
                                                                                                                                                                                                                                                                                                                                                                                           NADPH-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                    Methionine gamma-lyase; mdeA gene; free directed evolution; molecular breeding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic nucleotide sequence of a NADPH-dependent carbonyl reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-2001
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(BIOC-) BIOCATALYTICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTTACATCTACGGTCCTTTGACCAAG 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCAACGATCCTCAAAACCAAGTTGTCTACAACATGTCCAAGGCTGGTGTTATCCATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTTACATGGATACCGCCCTGAATAAG 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCAAGTCTCTTGCTGCCGAGTGGGCCAAGTACAACATCCGTGTTAACTGCATTTCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTAAGACTTTGGCTTGTGAATGGGCTAAGTACAACATCAGAGTTAATTCTTTAAACCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     735 BP; 136 A; 234 C; 183 G; 182 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                     2000US-00494921.
2000US-00734237.
                                                                                                                                                 2001WO-US003186.
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Pred. No. 7.4e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 folding energy; gene shuffling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is a crop plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>.</u>
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RESULT 7 AAF12302

AAF12302 standard; cDNA; 1146

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13-MAR-2001 AAF12302;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes a modified NADPH-dependent carbonyl CC reductase. The polymucleotide was modified using using the method of the C invention. The specification describes a method for designing a synthetic CC polymucleotide. The method comprises providing a starting polymucleotide, CC determining the predicted free energy of folding per base of the CC polymucleotide, modifying the polymucleotide by replacing a codon with a CC different codon to provide a modified polymucleotide, determining free CC energy of folding per base of the modified polymucleotides, and comparing CC this with that of the original polymucleotide. The method is useful for CC developing nucleic acid sequences that enhance expression of the encoded CC protein in a heterologous host. The design and preparation of the encoded CC synthetic genes are used in application of gene shuffling, directed CC evolution and molecular breeding methods. The method allows expression of CC evolution and molecular breeding methods. The method allows expression of CC spield such as commencially viable levels, in particular proteins with low that commercially viable levels, in particular proteins with low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Designing synthetic nucleic acid sequences for improved amplification expression in host cell, by comparing free energy of folding of a starting polynucleotide and a modified polynucleotide having a codon
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                                                                                                                                                                                                                                                                                                                                      CTAAGACTTTGGCTTGTGAATGGGCTAAGTACAACATCAGAGTTTAATTCTTTAAACCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAAAGAAGGTATCAAGGGTGCTTCTGTTTGTTTTGATTGGTTCTATGTCTGGTGCCATTG
ACGGTGGTTACAC 842
                                ATGGTGGTTTCAC
                                                                           ACCIGITICIGGCITCIGA-
                                                                                                                TTTTGTACTTGCTTTCTGAATCTGCTTCATACACTACTGGTGCCAGCTTACTGGTTG
                                                                                                                                                         GCTACATCAAC-----ACCGAAATCTCTGACTTTGTACCGCAGGAAACTCAGAACA
                                                                                                                                                                                                                                                                     GTTACATCTACGGTCCTTTGACCAAGAATGTTATCAATGGTAACGAAGAATTGTACAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                TCAACGATCCTCAAAACCAAGTTGTCTACAACATGTCCAAGGCTGGTGTTATCCATTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 104; 117pp;
                                                                                                                                                                                                                                                                                                              CTAAATCTCTGGCTGTAGAATTCGCTCCGT---TCGCTCGTGTTAACTCTGTTTCTCCGG
                                                                                                                                                                                                                                                                                                                                                                                           TTAACGTACCGCAGTTTCAGGCTACCTACAACGCTGCTAAAGCTGGTGTTCGTCACTTCG
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Pred. No. 4.4e-11;
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                                                                           -CGCTGGTTCTTACGCTACCGGCACTGACATCATCGTTG
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4.4e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FP) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Pusarium venenatum; AAF11248 to AAF1183 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus niger; AAF118579 to AAF15337 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOVO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monitoring differential
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                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coring differential expression fluorescence-labeled nucleic a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  esent invention describes a method for monitoring differential sion of genes in a first filamentous fungal (FF) cell relative sion of the same genes in one or more second filamentous fungal riche method uses fluorescence-labeled nucleic acids isolated from the method uses fluorescence-labeled nucleic acids.
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CTAATTGCGAGCATGAGTGGTACTATTGCCAATCGGGGTCTTATCTGCCCTGCTTACAAT
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Pred. No. 6
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microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                               The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a
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                                                        14-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a DNA construct comprising a promoter that functions in plants and selecting a desired plant from a population of transformed plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 17; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 containing the DNA construct.
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                       TGGTCGCGCTGGAGAGCCAAATGAGG---TTTCATCACTTGTGGCTTTTCTGTGTCTACC
                                                                                               ACAAAGAATGTCCGAACCAAAGGAATACATTGGTGCTGTTTTGTACTTGCTTTCTGAATC
                                                                                                                                 TCAACCTTTTTTCAAAG----ACGCCGATTACGAGAAGAGTTTGGTTAGTAGAACTCCACT
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Pred. No. 1.1e
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RESULT 10
ADS48180
                                                           Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; pathogen tolerance; plant growth regulator; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                      nitrogen;
                                                                                                                                                                                                                                                                     Bacterial polynucleotide #2923.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADS48180
                                  phosphorus; photosynthesis; lignin;
polymucleotide;
                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA;
gene; ss.
                                  galactomannan;
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704

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RESULT 11
AAF11343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprising the recombinant DNA construct and a method of producing a crop plant of transformed plant is a crop plant of transformed plant is a crop plant of transformed plant is a crop plant of such as maize or soybean. The method of producing a transformed plant construct and supported property. The plant is a crop plant of the property of the plant is a crop plant of the property of the plant is a crop plant of the plant of transformed plant with the construct and growing the transformed plant with the construct and growing the transformed plant where the construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plant properties. The recombination of protein pathogens or pests, concreased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of the cell cycle pathway with plant growth regulators, increased rate of condetent, improved yield by modified seed oil or protein yield and/or construct, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition. This sequence represents a bacterial polynucleotide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic forms from INSTOR of the printed specification of the production.
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                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 774 BP; 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a recombinant DNA construct comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 26610; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SLAT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2003
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AAF11343;
                                      AAF11343 standard; cDNA; 636 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  provide for expression of a polynucleotide encoding a polypeptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    format from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GOLD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HINK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CAOY/)
                                                                                                                                                                                                                                                                                                           436
                                                                                                                                                                                 592
                                                                                                                                                                                                                          496
                                                                                                                                                                                                                                                                                                                                                                                            102;
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) HINKLE G J.
) SLATER S C.
) CHEN X.
) GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hinkle GJ,
                                                                                                                                                                                                                                                                                                           ATCGCGTCCATGTCCGGACACATCGTGAACAAACCTCAGAAGCAGACAGCTTACAACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            functional
                                                                                                                                                                                 ATCAGAGTTAATTCTTTAAACCCCAGGTTACATCTACGGTCCTTTGA 637
                                                                                                                                                                                                                                                   TCCAAGGCTGGTGTTATCCATTTGGCTAAGACTTTGGCTTGTGAATGGGCTAAGTACAAC 591
                                                                                                                                                                                                                                                                                                                                           ATTGGTTCTATGTCTGGTGCCATTGTCAACGATCCTCAAAACCAAGTTGTCTACAACATG 531
                                                                                                                                                                                                                          TCGAAAGCGGGTGTGATCCATCTCACCAGATCTCTGGCCGCCGAGTGGGCCCCGTACGGA
                                                                                                                                          ATCAGGGTGAACAGCATAAGCCCCCGGATACATCAGAACACCTCTCA 60:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in a
                                                                                                                                                                                                                                                                                                                                                                                                           61.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; 160 C; 229 G; 159 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                              7.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant cell, where
                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 63.6; DB 13
Pred. No. 6.9e-08;
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                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the promoter is positioned
                                                                                                                                                                                                                                                                                                                                                                                              64;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 774;
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                                                                                                                                                                                                                                          The present invention describes a method for monitoring differential cc expression of genes in a first filamentous fungal (FF) cell relative to cells. The method uses fluorescence-tabeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS care used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of genes con a first filamentous fungal (FF) cell relative to expression of the ESTS confidence of genes in one or more second filamentous fungal cells. Monitoring the commence of the microorganisms to be improved. New genes may be discovered, conditions of genes from FF cells allows the production potential configurations of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, configuration of the expression conditions, environmental stress, spore morphogenesis, recombination of credundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 corporation from Aspergillus niger; AAF11854 to AAF11853 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from the present invention.
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                                                                                                                Query Match
Best Local Similarity
Matches 194; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombinate culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monitoring differential expression of genes in filamentous fungues fluorescence-labeled nucleic acids isolated from the cells substrate of expressed sequence tags.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus niger EST SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-594572/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berka RM, Rey MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multiple gene expression; filamentous fungal cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-2001
                                                                                                                                                                                           Sequence
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 CAAGTTGCTAAGGATTTTGGTAAGTTGCCATTGCACTTGGTTAACACAGCTGGTTACTGT 330
                                                                                                                                                                                         636 BP; 169 A; 155 C; 161 G; 149 T; 0 U; 2 Other;
                                       AAGTCAGCTGCCTATAAAGCTGATGTCGGAAATCAGGAGGATATTGAGAGGGTAATCCAG
                                                                             AAGATGGGTTCATATGCCTGTGATATTTCTGATTCTGATACCGTTCACAAGGTGTTTTGCT
                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shuster JR,
                                                                                                                                  7.4%;
51.3%;
                                                                                                                  0;
                                                                                                                  Score 60.6; DE
Pred. No. 4.7e-
0; Mismatches
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                                                                                                                                        4.7e-07
                                                                                                                                                          DB 3;
                                                                                                                      175;
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CAGATTGCTTCAGACTTTGGCAAGCTTGATATTATCGTCGTGAAC---TCGGGGGTCACT

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RESULT 12
AAL57425
ID AAL57
AC Optic
KW Optic
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KW tropic
KW tropic
CC Optic
CC Optic
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                                                                                                                                                                                                                                                                                                                          07-DEC-2001;
27-MAY-2002;
31-MAY-2002;
            This invention relates to a novel method for the preparation of an optically active alcohol by assymetric reduction of a ketone with a enzymatic material having tropinone reductase-1 activity, in the prof a reduced co-enzyme. Optically active alcohols are useful in the preparation of optically active compounds, for example (R)-3 quinuclidinol is an intermediate in the preparation of therapeutic agents. These can be used, for example, for the treatment of
                                                                                                                               Claim 9; Page 20-21; 30pp; English
                                                                                                                                                               cropinone
                                                                                                                                                                           Preparation of optically via asymmetric reduction
                                                                                                                                                                                                                                                                   Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                    06-DEC-2002; 2002EP-00027311
                                                                                                                                                                                                                                                                                                                                                                                                                                               BP1318200-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tropinone reducta
arteriosclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Datura
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DB; AAO27397.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGGTGCTTCTGTTTTGATTGGTTCTATGTCTGGTGCCATTGTCAACGATCCTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGITGGGTTCTTTGTATGTTTCTCAAGCCTTTGCTAAGCCATTGATCAAAGAAGGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCAATATCGCGGCAGAAGACTACACCACCGAACAATGGCGTGACATCATGAAGGTCAAT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAAACTTCCCATGTGAAGATTACCCAGCCAAGAACGCTGAGAAGATGGTGAAGGTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACCAAGTTGTCTACAACATGTCCAAGGCTGGTGTTATCCATTTGGCTAAGACTTTGGCT
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2002JP-00152955.
2002US-0385434P.
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   Co-expression
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                                                                                                                                                                          active alcohols, of a ketone, e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Datura stramonium tropinone reductase-1"
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RESULT 13
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Best Local S
Matches 158
     Arabinitol dehydrogenase gene encoding D-arabinitol dehydrogenase useful as a clinical diagnosing agent for mycosis.
                                                                                                          26-MAY-1998;
                                                                                                                                26-MAY-1998;
                                                                                                                                                      07-DEC-1999
                                                                                                                                                                            JP11332569-A
                                                                                                                                                                                                                                                                 Bacillus
                                                                                                                                                                                                                                                                                       D-arabinitol
                                                                                                                                                                                                                                                                                                             Bacillus D-arabinitol
                                                                                                                                                                                                                                                                                                                                   31-MAR-2000
                                                                                                                                                                                                                                                                                                                                                        AAZ46762;
                                                                         (NIPK )
                                                                                                                                                                                                                                                                                                                                                                              AAZ46762 standard; DNA; 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention, enables more efficient production of optically active alcohols. The present sequence is the Datura stramonium (jimsonweed, common thornapple) tropinone reductase-1 gene sequence. The protein encoded by this gene was utilised in the method of the invention
                                                  2000-091353/08
                                                                                                                                                                                                                                                                                                                                                                                                                                    807
                                                                                                                                                                                                                                                                                                                                                                                                                                                          813
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                                                                         IKEDA S
                                         AAY56815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                    T 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCCCTGCTGCTTCATATATTACGGGCCAGATCATATGGGCTGACGGTGGATTCACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAATCTGCTGCTTCATACACTACTGGTGCCAGCTTACTGGTTGATGGTGGTTTCACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACTCCTATGGGCCGGGCCGGAAAGCCCCCAAGAAGTTTCTGCACTAATAGCTTTTCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  822 BP; 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCACAACAAAGAATGTCCGAACCAAAGGAATACATTGGTGCTGTTTTGTACTTGCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAAACTGCAATTAAGAAAAATCCTCATCAAAAAGAAGAAATAGACAATTTTATTGTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGAATGTTATC-----AATGGTAACGAAGAATTGTACAACAGATGGATCTCTGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCTAAAGACAATTCGGGTCAATTCAGTTGCTCCGGGAGTCATTTTAACCCCACTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCTAAGTACAACATCAGAGTTAATTCTTTAAACCCAGGTTACATCTACGGTCCTTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTCTACAACATGTCCAAGGCTGGTGTTATCCATTTGGCTAAGACTTTGGCTTGTGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTTACTCAGCTTCCAAAGGTGCAATAAATCAAATGACAAAGAGTTTTGGCTTGTGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                     dehydrogenase;
                                                                                                                                                                                                                                                                                                                                  (first
                                                                                    SHOKKEN
                                                                         KAYAKU
                                                                                                          98JP-00143637
                                                                                                                                98JP-00143637.
                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                            /product= "D-arabinitol dehydrogenase"
/note= "the stop codon is not indicate
                                                                                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;
                                                                         ፭፭
                                                                                                                                                                                                                                                                                                           dehydrogenase coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 C;
                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                      clinical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59.8;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                     diagnosis; mycosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; DB
9e-07;
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RESULT 14
AAZ46763
ID AAZ46763
AC AAZ46
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Best Local Similarity 50.4
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to gene encoding D-arabinitol dehydrogenase, isolated from Bacillus sp. IKD-5A868 strain. The protein can be expressed by standard recombinant methodologies. D-arabinitol dehydrogenase is used as a clinical diagnosing agent for mycosis. The present sequence represents the coding sequence of the D-arabinitol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 774 BP; 155 A; 214 C; 271 G; 134 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 10-11; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D-arabinitol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus D-arabinitol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000
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                                                                                                                                                                                                                                                                             07-DEC-1999.
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                                                                                                                                                                                                                             26-MAY-1998;
                                                                                               (NIPK ) NIPPON KAYAKU
                                                                                                                                                                            26-MAY-1998;
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                         2000-091353/08
DB; AAY56815.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCGGCGTGTTCACGATTGACGGGGGCTATACGATTTGG
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                                                                                                                                                                            98JP-00143637
                                                                                                                                                                                                                          98JP-00143637
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                                                                                                                                                                                                                                                                                                                                                                          /product= "D-arabinitol dehydrogenase"
/note= "the coding segmence to store"
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Pred. No. 1.5e-06;
0; Mismatches 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isolated from Bacillus sp. IKD-5A868 strain. The protein can be expressed by standard recombinant methodologies. D-arabinitol dehydrogenase is used as a clinical diagnosing agent for mycosis. The present sequence represents the DNA encoding the D-arabinitol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2255 BP; 418 A; 623 C; 728 G; 486 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to gene encoding D-arabinitol dehydrogenase, isolated from Bacillus sp. IKD-5A868 strain. The protein can be ex-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabinitol dehydrogenase gene encoding D-arabinitol dehydrogenase useful as a clinical diagnosing agent for mycosis.
 1101
                                                                1043
                                                                                                                                                                                                                                                             864
                                                                                                                                                                                                                                                                                                                             804
                                778
                                                                                                718
                                                                                                                                984
                                                                                                                                                            658
                                                                                                                                                                                              924
                                                                                                                                                                                                                            598
                                                                                                                                                                                                                                                                                                                                                        TCTATGTCTGGTGCCATTGTCAACGATCCTCAAAACCAAGTTGTCTACAACATGTCCAAG
                                                                                                                              AACGAAGAATTGTAÇAACAGATGGATCTCTGGTATCCCACAACAAGAATGTCCGGAACCA
                                                                                                                                                                                            ĠŢĊĀĀĊĄĊĠĀŢŢĠĊĠĊĊĊĠĠĊŢĀĊĀŢĠĀĠŖĀĠĠĊŖĀĢĊĠĠĀĄĊĊĠŦĀŢŢŢĊĠĊĊĠĊĊ
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                                                                                                                                                                                                                                                                                         GCTGGTGTTATCCATTTGGCTAAGACTTTGGCTTGTGAATGGGCTAAGTACAACATCAGA
                                                                                                                                                                                                                                                                                                                         TCCATGTCGGGCCTGATCGTCAATACGCCGCAGCCGCAGGCGGCCTACAATGTCTCCAAG
                                                                                         AAGGAATACATTGGTGCTGTTTTGTACTTGCTTCTGAATCTGCTGCTTCATACACTACT
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 GGCGGCGTGTTCACGATTGACGGGGCTATACGATTTGG
                              GGTGCCAGCTTACTGGTTGATGGTGGTTTCACTTCTTGG
                                                                 --GCACGAGCTGGGCGGCATTGCGGTCTACCTTGCTTCGGACGCTTCCTCCTTCGCCACG
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            50.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                           7.2%;
                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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Pred. No. 2.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                  165;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2255;
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                                                                        1100
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25-FEB-1999 05-MAR-1999 09-MAR-1999 23-MAR-1999 25-MAR-1999 29-MAR-1999 01-APR-1999 06-APR-1999 AAC42189 standard; promoter; termination sequence; ss. Hybridisation assay; genetic mapping; gene e protein identification; signal transduction Arabidopsis thaliana DNA fragment 17-OCT-2000 Arabidopsis thaliana 25-FEB-2000; 2000EP-00301439 (first entry) 99US-0123180P 99US-0123548P 99US-0125788P 99US-0126264P 99US-0126264P 99US-0126768P 99US-0128234P 99US-0128714P 99US-0121825P DNA; 798 ₽₽ SEQ ID NO: expression control; n pathway; metabolic pathway; 34619

pathway;

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Search completed: July 12, Job time : 562 secs
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Sequence 2489, Ap
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Sequence 1675, Ap
Sequence 5, Appli
Sequence 7, Appli
Sequence 1, Appli
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Sequence 240, Ap
Sequence 71, Appl
Sequence 2654, Ap
Sequence 2488, Ap
Sequence 6987, Appl
Sequence 725, Appl
Sequence 27, Appli
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| ; | 40.8 | 40.8 | 41 | 41 | 41 | 41 | 41.2 | 41.4 | 41.4 | 41.4 | 42.2 | 42.2 | 42.2 | 43 | 43 | 43 | 43 | 43 |
| ; | 5.0 | 5.0 | 5.0 | 5.0 | 5.0 | 5.0 | 5.0 | 5.1 | 5.1 | 5.1 | 5.2 | 5.2 | 5.2 | 5.3 | 5.3 | 5. 3 | 5.3 | 5.3 |
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| 1 | Seguence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence |
| | 13563. A | 62984, A | 2671, Ap | 14, Appl | 14, Appl | 14, Appl | 148, App | 3426, Ap | 381, App | 1594, Ap | 4169, Ap | 3922, Ap | 3157, Ap | 17, Appl | • | 17, Appl | • | 22, Appl |

ALIGNMENTS

Sequence 6, Application
Patent No. 586382
GENERAL INFORMATION:
APPLICANT: Hallborr
APPLICANT: Penttila
APPLICANT: Ojamo, H
APPLICANT: Keranen,
APPLICANT: Hahn-Hag RESULT 1 US-08-336-198C-6 TELEFAX: 703-205-8050 TELEX: 248345 INFORMATION FOR SEQ ID NO: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,198C
PILING DATE: 03-NOV-1994
CLASSIFICATION: 435 TOPOLOGY: 11near MOLECULE TYPE: CDN SEQUENCE CHARACTERISTICS: LENGTH: 696 base pairs TYPE: nucleic acid STRANDEDNESS: double ATTORNEY/AGENT INFORMATION:
NAME: MULPPHY JT., Gerald M.
REGISTRATION NUMBER: 28,977
TELECOMMUNICATION INFORMATION: CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 N. Washington St.
CITY: Falls Church
STATE: Virginia HYPOTHETICAL: NO ORIGINAL SOURCE: NUMBER OF SEQUENCES: APPLICANT: Hahn-Hagerdal, Barbei APPLICANT: Waldfridsson, Mats APPLICANT: Airaksinen, Ulla TITLE OF INVENTION: XYLOSE UTILIZATION BY RECOMBINANT YEASTS ORGANISM: Pichia stipitis STRAIN: CBS-6054 ZIP: 22046-3487 NAME/KEY: CDS TELEPHONE: COUNTRY: 6, Application US/08336198C o. 5866382 USA Keranen, Sirkka Penttila, Merja Ojamo, Heikki linear 703-205-8000 CDNA 6. Version #1

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PUBLICATION INFORMATION:

DOCUMENT NUMBER: FI 901771

FILING DATE: 06-APR-1990

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; Sequence 6, Application US/09184965
; Patent No. 6582944
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Best Local Similarity
Matches 373; Conserv
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APPLICANT:
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                                                                             APPLICANT: Hahn-Hagerdal, Barbei
APPLICANT: Waldfridsson, Mats
APPLICANT: Airaksinen, Ulla
TITLE OF INVENTION: XYLOSE UTILIZATION
NUMBER OF SEQUENCES: 9
                                                                CORRESPONDENCE ADDRESS:
STREET: 301 N. Washington CITY: Falls Church STATE: Virginia
                                                ADDRESSEE:
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Penttila, Merja
Ojamo, Heikki
Keranen, Sirkka
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0; Mismatches 203;
                                                Kolasch & Birch
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
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OTHER INFORMATION: /standard
OTHER INFORMATION: dehydroge
PUBLICATION INFORMATION:
DOCUMENT NUMBER: FI 901771
FILING DATE: 06-APR-1990
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
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LENGTH: 696 base pairs
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APPLICATION NUMBER: US/0:
FILING DATE: 03-NOV-1994
ATTORNEY/AGENT INFORMATION:
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TELEFAX: 248345
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STRAIN: C
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LOCATION:
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                       ACAACATCAGAGTTAATTCTTTAAACCCAGGTTACATCTACGGTCCTTTGACCAAGAATG
                                                                                     ACATGTCCAAGGCTGGTGTTATCCATTTGGCTAAGACTTTGGCTTGTGAATGGGCTAAGT
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Pred. No. 9.4e-65;
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APPLICANT: Keith Weinstock et al
ITITLE OF INVENTION: NUCLEIC ACID AND AMINO AC
ITITLE OF INVENTION: NUCLEIC ACID AND THER
ITITLE OF INVENTION: FOR DIAGNOSTICS AND THER
PILE REFERENCE: 107196.132
CURRENT FILING DATE: 199-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
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ORGANISM: Candida
-09-248-796A-29
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                                                       CTAGACCATTAATCCAAAA----CAACATGACCGGATCGATCATTTTGATCGGGTCAATGT
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT PILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 2490
LENGTH: 927
TWORLD TANK
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                   ATCCGGATGTCAAGAGTAAATGGTTGCAACTTACACCACTTGGTAGAGAAGCCAAACCAA
                                                                                                                          TTAATTCTTTAAACCCAGGTTACATCTACGGTCCTTTGACCAAGAATGTTATCAATGGTA
                                                                                                                                                                 CTGGGGTCAAACATTTGTCCAAATCATTGAGTGTTTGAATGGGCACCATTTGCT---AGAG
                                                                                                                                                                                                  CTGGTGTTATCCATTTGGCTAAGACTTTGGCTTGTGAATGGGCTAAGTACAACATCAGAG
                                                                                                                                                                                                                                        GTATGTCGGCTTCAATTGTTAATGTCCCACAATTACAAGCAGCTTACAACGCTGCTAAAG
                                                                                                                                                                                                                                                                           CTATGTCTGGTGCCATTGTCAACGATCCTCAAAACCAAGTTGTCTACAACATGTCCAAGG
                                                                                                                                                                                                                                                                                                               TTGTTGGTCCAATTTTCAGAAAAAAGGGTA-----AAGGGTCATTCATTTTCACTGCCA
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                                                     ACGAAGAATTGTACAACAGATGGATCTCTGGTATCCCACAACAAAGAATGTCCGAACCAA 718
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Pred. No. 8.1e-17;
0; Mismatches 279
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658 769

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APPLICANT: Hus, Ling
ITITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED EXI
FILE REFERENCE: B583:40608
CURRENT APPLICATION NUMBER: US/09/734,237B
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/494,921
PRIOR FILING DATE: 2000-01-31
NUMBER: 09/8040,921
PRIOR FILING DATE: 2000-01-31
NUMBER: OF SEQ ID NOS: 79
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 71
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US-09-248-796A-2654

IS-09-248-796A-2654; Sequence 2654; Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:
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OTHER INFORMATION:
US-09-734-237B-71
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Best Local S
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APPLICANT: Bui, Peter
APPLICANT: Hua, Ling
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                               GATGGATCTCTGGTATCCCACAACAAAGAATGTCCGAACCAAAGGAATACATTGGTGCTG
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                                                                                                                                                                                  ACCTGTTTCTGGCTTCTGA---CGCTGGTTCTTACGCTACCGGCACTGACATCATCGTTG
                                                                                                                                                                                                               TTTTGTACTTGCTTTCTGAATCTGCTGCTTCATACACTACTGGTGCCAGCTTACTGGTTG
                                                                                                                                                                                                                                                 GTTACATCTACGGTCCTTTGACCAAGAATGTTATCAATGGTAACGAAGAATTGTACAACA
                                                                                                                                                                                                                                                                                                                                                                                                             CTAAGACTTTGGCTTGTGAATGGGCTAAGTACAACATCAGAGTTAATTCTTTAAACCCAG
                                                                                                                                                    ATGGTGGTTTCAC 809
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Pred. No. 4.7e-13;
0; Mismatches 149;
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US-09-248-796A-2488

Sequence 2488, Application US/09248796A Patent No. 6747137

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12

RELATING

TO CANDIDA ALBICAN

PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13

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PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 2654
LENGTH: 873
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Best Local
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CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
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                                                                                                                            ATTGTTGÁT-----TTGAGAATCCCAATGAAAAGATGGGGTAACCCAGACGACTTT
                                                                                                                                                                                                                    TTAAACCCAGGTTACATCTACGGTCCTTTGACCAAGAATGTTATCAATGGTAACGAAGAA
                                                                                                                                                                                                                                                                                        ATCCATTTGGCTAAGACTTTGGCTTGTGAATGGGCTAAGTACAACATCAGAGTTAATTCT
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                                                                                            ATTGGTGCTGTTTTGTACTTGCTTTCTGAATCTGCTTCATACACTACTGGTGCCAGC
                                                                                                                                                          TTGTACAACAGATGGATCTCTGGTATCCCACAACAAAGAATGTCCGAACCAAAGGAATAC
                                                                                                                                                                                              ATTGCACCTGGATATATCAAAACCAATTTGACCGACAGCATGAGTGAAGAGAACAAGAAA
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 TTATTAGTTGATGGTGGTT
                              TTACTGGTTGATGGTGGTT
                                                            ATGGGGCCAATTGTCTATCTTACATCTGA--
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51.3%;
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Pred. No. 5.3e-09;
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                                                                   TĠĊATĊGAAATATGTTAĊTĠĠTĠAĊĀCA
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LENGTH: 336
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                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                            SEQ ID NO 6987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6987, Application US/09248796A Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 171; Conserv
                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
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                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                           LENGTH: 372
TYPE: DNA
ORGANISM: Candida albicans
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ORGANISM: Candida albicans
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Similarity 62.4%;
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                             ACCAAGAAAAGAC 146
ACTTGGAAAGAAC
                                                        CTGCCGTGGTATCAAGAGCTTTATTAGCCAAAGGTGCCGATGTTGCATTAGTCGATATGA 86
                                                                                                                    TCCCAAGCTTCCGTTTGGATGGAAAACTAGTCATATTAACCGGTGGCTCTGGTGGTTTGG
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Pred. No.
                                                                                                                                                                                              Score 53; DB 4;
Pred. No. 2e-06;
                                                                                                                                                                                 Mismatches
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RESULT 10 US-09-248-796A-2730

Sequence 2730, Application US/09248796A Patent No. 6747137

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725

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SEQ ID NO 725
LENGTH: 774
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
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PRIOR APPLICATION NUMBER: US 60/055,779
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                                ACATCTACGGTCCTTTGACCAAGAATGTTATCAATGGTAACGAAGAA
                                                                         AAAGCTTAGCTAGAGAATGGTCTAGATATGGAATTAAAGTAAATGCAATTGCCCCTGGTT
                                                                                                          AGACTTTGGCTTGTGAATGGGCTAAGTACAACATCAGAGTTAATTCTTTAAACCCCAGGTT
                                                                                                                                              ATAAAACGCAAGACCAGAGCTCTTATGAAACGTCTAAAGCCGGTGTGACGATGCTGACTA
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ACATGAGAACAATCGAAACGGAAAAGATACTAAATGATAATACTGAA
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Pred. No. 3e-06
0; Mismatches
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; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2730
LENGTH: 825
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-2730
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US-09-367-012-2
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Best Local Similarity
Matches 299; Conserv
                                                                                                                                                           Sequence 2, Application US/09367012 Patent No. 6218156
                                                                                                                                            GENERAL INFORMATION:
                                                         APPLICANT: Yasohara, Yoshi
APPLICANT: Kizaki, No. 6216
APPLICANT: Hasegawa, Junzo
APPLICANT: Wada, Masaru
APPLICANT: Shimizu, Sakayu
                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376
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                                             Shimizu, Sakayu
Kataoka, Michihiko
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             Yamamoto, Kazuhiko
Kawabata, Hiroshi
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; TYPE: DNA; Candida magnoliae US-09-367-012-2
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US-09-777-157A-2
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Best Local S
Matches 89
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 852
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SEQ ID NO 2
SERVER B52
TYPE: DNA
ORGANISM: Candida magnoliae
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Patent No. 644805
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                                                                                                                                                                Matches
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CURRENT APPLICATION NUMBER: US/09/777,157A
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/367,012
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 8
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Local Similarity 58.6%;
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Kawabata, Hiroshi
Kita, Keiko
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CTAAGACTTTGGCTTGTGAATGGGCTAAGTAC
                                 TGAACGTGCCCCAGTTCCAGGCCACGTACAACGCGGCCAAGGCTGGCGTGCGCCACTTCG
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Katoka, Michihiko
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Pred. No. 1.
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Pred. No. 1.2e-05;
0; Mismatches 63
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US-09-734-237B-69
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PRESUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT FILING NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 5819
LENGTH: 951
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Matches
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GENERAL INFORMATION:
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                                                                                                                                                                              Query Match
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Best Local Similarity
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ORGANISM: Klebsiella pneumoniae
-09-489-039A-5819
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PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 79
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CURRENT APPLICATION NUMBER: US/09/734,237B
CURRENT FILING DATE: 2000-12-08
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APPLICANT: Hua, Ling
TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED EXPRESSION
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TYPE: DNA
ORGANISM: Candida magnoliae
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514 CAAGTTGTCTACAACATGTCCAAAGGCTGGTGTTATCCATTTTGGCTAAGACTTTTGGCTTGT 573
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                                                                                                                                                          Similarity
                                                             GGCGGGTCGATTATCAATATCGCCTCGATGTCGGGGATTATTGTTAACCGCGGCCTCGAC
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Pred. No. 1.2e-05;
0; Mismatches 83;
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Search completed: July 12, 2005, 15:30:36 Job time: 191 secs

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; TYPE: DNA
; ORGANISM: Candida magnoliae
US-09-367-012-8
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US-09-367-012-8
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SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/367,012
CURRENT FILING DATE: 1999-11-24
EARLIER APPLICATION NUMBER: PCT/JP97/03051
EARLIER FILING DATE: 1997-09-01
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yasohara, Yoshir
APPLICANT: Kizaki, No. 6218
APPLICANT: Hasegawa, Junzo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: No. 6218156el carbonyl reductase, TITLE OF INVENTION: for using such reductase and gene FILE REFERENCE: $72030PCUS
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APPLICANT: Kataoka, Michihiko
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APPLICANT: Kawabata, Hiroshi
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763
                                                                                                                                               643 TCGAGAAGGAGGCAAGAAGGGCGCCCTTGTGTTCACGGCCTCCATGTCTGGCCACATTG
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                                                                                                   TCAACGATCCTCAAAACCAAGTTGTCTACAACATGTCCAAGGCTGGTGTTATCCATTTGG
CGAAGTCGCTGGCCGTCGAGTTCGCGCCGTTC
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                                CTAAGACTTTGGCTTGTGAATGGGCTAAGTAC
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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99.4
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/cgn2_6/ptodata/2/pubpna/US09 NEW PUB.seq:*
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687
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26/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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26/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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    US-10-720-018-1

US-10-653-047-41

US-10-653-047-4932

US-10-369-493-36723

US-10-369-493-26991

US-09-734-237B-71

US-10-653-047-4825
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Sequence 41, Appl
Sequence 4932, Ap
Sequence 36723, A
Sequence 26991, A
Sequence 71, Appl
Sequence 4825, Ap
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ALIGNMENTS

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US-10-720-018-1
                                                                                                                                                                                                                                                                                             APPLICANT: Verho, Ritva
APPLICANT: Richard, Peter
APPLICANT: Richard, Peter
APPLICANT: Penttila, Merja
TITLE OF INVENTION: New Enzyme for an in vivo and in vitro Utilisation
TITLE OF INVENTION: Carbohydrates
FILE REFERENCE: 2530-120
CURRENT APPLICATION NUMBER: US/10/720,018
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 6
SOFTWARB: PatentIn version 3.2
SEQ ID NO 16
                                                                                                                               Query Match
Best Local Similarity
Matches 816; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/10720018
Publication No. US20040132074A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Ambrosiozyma monospora
                                                                                                                                                                                                                                                              LENGTH: 816
TYPE: DNA
TGTGGTGGTTTAGCTGAAGCTTTAATCAAGGGTTTGTTGGCCTACGGTTCTGACATTGCT 120
                                                                                    ATGACTGACTACATTCCAACTTTTAGATTCGATGGCCACTTAACCATTGTCACAGGTGCC 60
                                                                                                                               100.0%; Score 816; DB 19; ilarity 100.0%; Pred. No. 2.4e-230; Conservative 0; Mismatches 0;
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APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R.Shuster
APPLICANT: Sakari Kaupinen
APPLICANT: Sakari Kaupinen
APPLICANT: Ib Groth Clausen
APPLICANT: Ib Groth Clausen
APPLICANT: Peter Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Gen
TITLE OF INVENTION: Expression
FILE REFERENCE: 5849-200-US
CURRENT APPLICATION NUMBER: US/10/653,047
CURRENT APPLICATION NUMBER: US/10/653,047
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US/09/533,559
PRIOR APPLICATION NUMBER: 09/273,623
PRIOR FILING DATE: 1099-03-22
PRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
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                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Randy M.
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 Sequence 4932, Application US/10653047

Publication No. US20040229367A1

GENERAL INFORMATION:
APPLICANT: Michael W. Rey
APPLICANT: Michael W. Rey
APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R. Shuster
APPLICANT: Ib Groth Clausen
APPLICANT: Ib Groth Clausen
APPLICANT: Peter Bjarke Olsen
APPLICANT: Peter Bjarke Olsen
APPLICANT: Peter Bjarke Olsen
FITLE OF INVENTION: Methods For Monitoring Multiple Gen
FITLE OF INVENTION: Expression
FILE REFERENCE: 5849.200-US
CURRENT APPLICATION NUMBER: US/10/653,047
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US/09/533,559
PRIOR APPLICATION NUMBER: US/09/533,559
PRIOR APPLICATION NUMBER: US/09/533,559
PRIOR APPLICATION DATE: 2000-03-22
PRIOR APPLICATION DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
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, NAME/KEY: misc_feature
; LOCATION: (1): ... (3203)
; OTHER INFORMATION: n = A,T,C
US-10-653-047-41
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US-10-653-047-4932
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SEQ ID NO 41
LENGTH: 3203
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TYPE: DNA
ORGANISM: Fusarium
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TGCGCAAGTTGTGGGGTGTTAATGTTGACGGTACTTACCTCTTTGCAGTTGCAGTTGCCA
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TTAGAGTAGATGGAGGATATACT 3109
                                TACTGGTTGATGGTGGTTTCACT
                                                                                     TGGGTCCTGT----GACCTTTTTGTTGCAGATGCGTCTTCTTACATGACTGGGGCAGATC 3086
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Pred. No. 4.5e-18;
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Sequence 36723, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: DIANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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US-10-369-493-36723
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; LOCATION: (1)...(687)
; OTHER INFORMATION: n = A,T,C or
US-10-653-047-4932
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Best Local Similarity
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SEQ ID NO 4932
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Pred. No. 2.9e-15;
0; Mismatches 275;
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Coldman, Barry S.
APPLICANT: Chen, Xianfeng
ITITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN EXPERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
RIOR APPLICATION NUMBER: US 60/360,039
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 26991
LENGTH: 735
TYPE: DNA
ORGANISM: Neurospora crassa
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US-10-369-493-26991
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; SEQ ID NO 36723
; LENGTH: 637
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-10-369-493-36723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26991, Application US/10369493
Publication No. US20030233675A1
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Best Local Similarity
Matches 183; Conserv
                                                                                                                                                                                    Matches 128;
                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                      Local Similarity
                                                                                                                                  436 ATCAAAGAAGGTATCAAGGGTGCTTCTGTTTGTTTTGATTGGTTCCTATGTCTGGTGCCATT 495
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556 GCTAAGACTTTGGCTTGTGAATGGGCTAAGTACAACATCAGAGTTAATTCTTTAAACCCA 615
                                                                       496 GTCAACGATCCTCAAAACCAAGTTGTCTACAACATGTCCAAGGCTGGTGTTATCCATTTG 555
                                                                                                            364 ATGATGGCCGCTGGCAAACCCGGCTCCATTATCCTTGTTGCCTCGATGTCCGGCACCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 CACTTGGTTAACACAGCTGGTTACTGTGAAAACTTCCCATGTGAAGATTACCCAGCCAAG
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                                    GTCAACTACCCTCAGGAGCAGTCGTGCTACAACGCCTCTAAGGCTGGTGTCATTCAGCTC
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                                                                                                                                                                                  Score 80.6; DB 17;
Pred. No. 7e-13;
0; Mismatches 79;
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Pred. No. 2.8e-13;
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US-10-653-047-4825
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Sequence 4825, Application US/10653047
Publication No. US/20040229367A1
GENERAL INFORMATION:
APPLICANT: Randy M. Berka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 71, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Sim Matches 209;
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APPLICANT: Bui, Peter
APPLICANT: Hua, Ling
APPLICANT: Hua, Ling
TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED
FILE REFERENCE: B583:40608
CURRENT FILING LATIEN UMBER: US/09/734,237B
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/494,921
PRIOR FILING DATE: 2000-01-31
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Synthetic gene derived from Candida magnoliae NADPH-dependent of OTHER INFORMATION: bonyl reductase, having numerous codons replaced with others en OTHER INFORMATION: ding the same amino acids to reduce the free energy of folding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 4.5e-11;
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                                                              APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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LENGTH: 1146
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 172450
LENGTH: 775
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                                                                                                                                                                                                                                                                                       Sequence 172450, Application US/10425115
Publication No. US20040214272A1
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PRIOR APPLICATION NUMBER: US/09/533,559
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/273,623
PRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOPTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Jeffrey R. Shuster
APPLICANT: Sakari Kauppinen
APPLICANT: Ib Groth Clausen
APPLICANT: Ib Groth Clausen
APPLICANT: Peter Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 5849.200-US
CURRENT APPLICATION NUMBER: US/10/653,047
CURRENT FILING DATE: 2003-08-29
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Conservative
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Pred. No. 7e-11;
0; Mismatches 198;
                                                                                                                                                             and Other Molecules Associated With
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                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-25810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-369-493-25810
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                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 25810
LENGTH: 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25810, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                                                            Query Match
Best Local 9
                                                                                                                                                                                                                                Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cao, Yongwei APPLICANT: Hinkle, Gre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Clone ID: MRT4577_88858C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
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                                                                                                                                                                                                  171 CAPATACGCTACTGAAGAATTGAAGTTGAAAGAAGTTCCAAAGATGGGTTCATATGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136;
                                                                                                                                                                                                                                              Similarity
                                                                                  TAAGTTGCCATTGCACTTGGTTAACACAGCTGGTTACTGTGAAAACTTCCCATGTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hinkle, Gregory J. Slater, Steven C. Soldman, Barry S. Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                    TTACCCAGCCAAGAACGCTGAGAAGATGGTGAACGTTAACTTGTTTGGGTTCTTTGTATGT 410
                                                                                                             CGATGTCACTATTCCTAAAGAGGTAGAACATGCCTTTGCTGAGATTCAAAAGGTCTTTGA
                                                                                                                                        TGATATTTCTGATTCTGATACCGTTCACAAGGTGTTTGCTCAAGTTGCTAAGGATTTTGG
                                                                                                                                                                      CGAAAAGGCTGCAAAGGAAATTGCCCCAGGCTAATGGTGTCAAGACTTATACATGCAAGTG
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CATGACTTACGAAGAATTTGCTAATGAAATAAACGTCAACTTGCTCGGTGTCTTCAACGT
                                                       TACTATTGATATCGTTGTGCCCAACAACGGTATTTGCACTGGCAAGTCCGCCATT---GA
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Pred. No. 5.1e-09;
0; Mismatches 194
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Pred. No. 1.9e-10;
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                                                                                                                                                                                                                                                        DB 17;
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                                                                                                                                                                                                                                                        Length 783;
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Slater, Gregory J.

FILCANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR OF SEQ ID NOS: 47374

SEQ ID NO 26610

LENGTH: 774
                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA; ORGANISM: Thermotoga maritima US-10-369-493-26610
                                                                                                                                                                                                                                                                      7.8%;
Best Local Similarity 61.4%;
Matches 102; Conservation
                                               592
                                                                                                                                             532
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                                          ATCAGAGTTAATTCTTTAAACCCAGGTTACATCTACGGTCCTTTGA
                                                                                                                                          TCCAAGGCTGGTGTTATCCATTTGGCTAAGACTTTGGCTTGTGAATGGGCTAAGTACAAC 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCCAAGGCTGGTGTATCCATTTGGCTAAGACTTTTGGCTTGTGAATGGGCTAAGT 586
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ATCAGGGTGAACAGCATAAGCCCCCGGATACATCAGAACACCTCTCA
                                                                                              TCGAAAGCGGGTGTGATCCATCTCACCAGATCTCTGGCCGCCGAGTGGGCCCCGTACGGA 555
                                                                                                                                                                                         ATCGCGTCCATGTCCGGACACATCGTGAACAAACCTCAGAAGCAGACAGCTTACAACGCT 495
                                                                                                                                                                                                                                        ATTGGTTCTATGTCTGGTGCCATTGTCAACGATCCTCAAAACCAAGTTGTCTACAACATG 531
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                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                        Score 63.6; DB 17
Pred. No. 7.7e-08;
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                                                                                                                                                                                                                                                                                                                                 DB 17;
                                                                                                                                                                                                                                                                                                                                 Length
                                               637
601
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RESULT 11

US-10-653-047-3866

US-10-653-047-3866

Sequence 3866, Application US/10653047

Sequence 3866, Application US/10653047

Publication No. US20040229367A1

GENERAL INFORMATION:

APPLICANT: Michael W. Rey

APPLICANT: Michael W. Rey

APPLICANT: Sakari Kauppinen

APPLICANT: Sakari Kauppinen

APPLICANT: Peter Bjarke Olsen

TITLE OF INVENTION: Methods For Monitoring Multiple Gene

TITLE OF INVENTION: Expression

FILE REFERENCE: 5849-200-US

CURRENT APPLICATION NUMBER: US/10/653,047

CURRENT APPLICATION NUMBER: US/09/533,559

PRIOR APPLICATION DATE: 2000-03-22
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PRIOR APPLICATION NUMBER: 09/273,623
PRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARR: FASSEQ for Windows Version 4.0
SEQ ID NO 3866
LENGTH: 636
TYPE: DNA
ORGANISM: Aspergillus niger
PRETURE:
PAME/KEY: misc feature
LOCATION: (1)...(636)
OTHER INFORMATION: n = A,T,C or G
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US-10-314-394-1
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US-10-314-394-1
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10314394 Publication No. US20030143700A1 GENERAL INFORMATION:
                                                SOFTWARE: PatentIn
SEQ ID NO 1
LENGTH: 822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/314,394
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: US 60/385,434
PRIOR FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: UP 2002-152955
PRIOR FILING DATE: 2002-05-27
PRIOR APPLICATION NUMBER: UP 2001-375041
                                                                                                                                                                                                                                                           APPLICANT: Hamatani, Takeshi
TITLE OF INVENTION: METHODS FOR PRODUCING OPTICALLY ACTIVE ALCOHOLS
FILE REFERENCE: SHZ-006
FILE REFERENCE: SHZ-006
                                                                                                       PRIOR FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yamamoto, Hiroaki
APPLICANT: Ueda, Momoko
               TYPE: DNA
ORGANISM: Datura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 AAGATGGGTTCATATGCCTGTGATATTTCTGATTCTGATACCGTTCACAAGGTGTTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 GAAAACTTCCCATGTGAAGATTACCCAGCCAAGAACGCTGAGAAGATGGTGAAGGTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 AAGTCAGCTGCCTATAAAGCTGATGTCGGAAATCAGGAGGATATTGAGAGGGTAATCCAG
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                                                                                                                                                                                                                                                                                                                                Ueda, Momoko
Pan, Ritsuzui
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               stramonium
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51.3%;
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; ORGANISM: Hyoscyamus niger
US-10-314-394-3
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US-10-314-394-3
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CURRENT APPLICATION NUMBER: US/10/314,394
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: US 60/385,434
PRIOR FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: JP 2002-152955
PRIOR FILING DATE: 2002-05-27
PRIOR APPLICATION NUMBER: JP 2001-375041
PRIOR APPLICATION NUMBER: JP 2001-375041
PRIOR FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 10
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Publication No. US20030143700A1
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 151; Conserv
                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hamatani, Takeshi
TITLE OF INVENTION: METHODS FOR PRODUCING OPTICALLY ACTIVE ALCOHOLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yamamoto, Hiroaki
APPLICANT: Ueda, Momoko
APPLICANT: Pan, Ritsuzui
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AAGAAAATCCTCATCAAAAAGAAGAATAGACAATTTTATTGTCAAGACTCCAATGGGC
                                                                                                                                                            TCCAAGGCTGGTGTTATCCATTTGGCTAAGACTTTGGCTTGTGAATGGGCTAAGTACAAC
                                                                      ATTCGGGTCAATTCAGTTGCTCCAGGAGTCATTTTAACCCCACTCATTGAAACTGCAATT
                                                                                                       ATCAGAGTTAATTCTTTAAACCCAGGTTACATCTACGGTCCTTTGACCAAGAATGTTATC
                                    ----- AATGGTAACGAAGAATTGTACAACAGATGGATCTCTGGTATCCCACAACAAGA
                                                                                                                                          TCCAAAGCTGCAATAAATCAAATAACGAAGAACTTGGCATGTGAATGGGCCAAGGACAAC
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Pred. No. 1.1e-06;
0; Mismatches 137;
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                                                                                                                                                                                                                             Score 56.4; DB 15; Pred. No. 1.1e-05;
                                                                                                                                                                                                                 Mismatches 131;
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US-09-938-842A-948
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CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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                                                                                                                                              Sequence 948, Application US/09938842A Publication No. US20040009476A9 GENERAL INFORMATION:
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LENGTH: 789
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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Best Local Similarity
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE: FILE REFERENCE; SCRIP1300-3
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                                                                                                                                                                                                                                                                                                                                CTACTGGTGCCAGCTTACTGGTTGATGGTGGTTTCAC 809
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Zhu, Tong
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Pred. No. 1.2e-05;
0; Mismatches 118;
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CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR PPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-22
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SEQ ID NO 948
LENGTH: 789
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 153;
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Best Local Similarity 55.2%;
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                                           CTACTGGTGCCAGCTTACTGGTTGATGGTGGTTTCAC 809
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Gaps

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661

Search completed: July 12, 2005, 15:54:44 Job time: 640 secs

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| | 7.8 | 7.8 | 7.9 | 8.0 | 8.0 | 8.2 | 8.3 | 8.3 | 8.3 | 8.6 | 8.6 | 8.7 | 8.7 | 8.8 | 8. 9 | 8.9 | 8.9 | 9.0 | 9.1 | 9.1 | 9.3 |
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REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 CNS077V0 LOCUS DEFINITION pichia angusta Pichia angusta Pichia angusta Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia. 1 (bases 1 to 899) Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottler, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potler, S. Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000) CNS077V0 899 bp DNA linear GSS 08-JUL-20 T7 end of clone BB0AA014G11 of library BB0AA from strain CBS 4732 of Pichia angusta, genomic survey sequence. AL433186.1 GI:12216600 GSS. Llorente, B., D., Potier, S., GSS 08-JUL-2001

ALIGNMENTS

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS 11152876

A set of

Genomi 2 (bases 1 to 899) Blandin, G., Llorente, B., Malpertuy, A., Wincker, P., Artiguenave, F. and Dujon, B ic exploration of the hemiascomycetous yeasts:

Genoscope. FEBS Lett. 20584723 11152888 (bases 1 to 899) 487 (1), 76-81 (2000)

REFERENCE

AUTHORS TITLE

Direct Submission

JOURNAL

JOURNAL MEDLINE PUBMED

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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefagenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of

COMMENT

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14-JUN-2004

Robert, L.S.,

K1A 0C6,

Couroux, P.,

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/strain="CBS 4732"
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YPK2; ser/thr protein kinase]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 276.6; DB 9;
Pred. No. 3.6e-68;
D; Mismatches 210;
                                                 816
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kinase ]"
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Best Local
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FG044 02e10 A
FG04 AAFC ECORC Fusarium graminearum mycelium grown on wheat heads
Gibberella zeae cDNA clone FG044 02e10, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: (613) 759-1658
Fax: (613) 759-1701
Email: ouellettr@agr.gc.ca.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Ouellet, Therese
Bastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Neatby Bldg., Central Experimental Farm, Ottawa, Ontario,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusarium graminearum mycelium grown humidity conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouellet, T., Koul, A., Dan, H., Harris, L.J., Chapados, J., De Moors, A., Hattori, J., Lacroix, C., Masotti, M., Rober Singh, J.A., Sprott, D. and Tinker, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 959)
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CD457882.1 GI:31372622
EST.
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                                                                                                                                                               TCTGGTGCCATTGTCAACGATCCTCAAAACCAAGTTGTCTACAACATGTCCAAGGCTGGT
                                                                                                                                                                                                              CCAGGCACTTGATGCAAAGAAAGGCTCCTGGTAGCATC----GTCATGATTGGTAGCATG
                                                                                                                                                                                                                                        CTAAGCCATTGAT-CAAAGAAGGTATCAAGGGTGCTTCTGTTTTTGATTGGTTCTATG
                                                                                                                                                                                                                                                                                    GTCTCCGTAAGCTTTGGGCTGTTAACGTTGACGGTACATATCTCTTTGCAACATCAGTCG
                                                                                                                                                                                                                                                                                                            ACGCTGAGAAGATGGTGAAGGTTAACTTGTTGGGTTCTTTGTATGTTTCTCAAGCCTTTG
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                                                                                                                                                                                                                                                                                                                                                                              ACTTGGTTAACACAGCTGGTTACTGTGAAAACTTCCCATGTGAAGATTACCCAGCCAAGA 364
TGCATCTCTCCCGGTTACATGTTGACTGCACTCACTCAGAAGATTCTTGACGACAACCCG
                                                                     GTGCGCCATCTCGCTGCTTTGGCCGTCGAATGGGCTCAGGCAAACATCCGAGTCAAC
                                                                                                 GTTATCCATTTGGCTAAGACTTTGGCTTGTGAATGGGCTAAGTACAACATCAGAGTTAAT
                                  TCTTTAAACCCAGGTTACATCTACGGTCCTTTGACCAAGAATGTTATCAATGGTAACGAA
                                                                                                                                            TCCGGATCCATTGTCAACGTTCCTCASCCTCAGGCTCCCTATAATGCCGCCAAAGCCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="Fg04 AAFC_ECORC_Fusarium_graminearum_mycelium_grown_on_wheat_heads"
grown_on_wheat_heads"
/note="Vector: Bluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Fusarium grown on wheat (cv. Roblin) under high
humidity. cDNA made using Stratagene kit."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="Fg04d 02e10"
/tissue type="Mycelium"
/dev_stage="Asexual"
/lab_host="E. coli"
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/strain="DAOM 180378"
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Pred. No. 1.1e-25;
3; Mismatches 206;
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Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harris, L.J., Glassco, T., Rocheleau, H., Allard, S., (Couroux, P., De Moors, A., Hattori, J.I., Ouellet, T., Singh, J.A, Sprott, D. and Tinker, N.A.

Expressed Sequence Tags from Fusarium graminearum (Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI750180 682 bp mRNA linear EST 14-
F902_10b03_R F902_AAFC_ECORC_FUSARIUM_graminearum_mycelium
Gibberella zeae cDNA clone F902_10b03, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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                                                                                                                                                              Similarity
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                                              CTGAAGCTTTAATCAAGGGTTTGTTGGCCTACGGTTCTGACATTGCTTTGCTTGATATCG 133
                GTCTTGTTATGGGTCAAGGAATGGTATTCTCTGGATCCAACCTTGCTCTTGTTGATATTW 139
                                                                                                           TTCCAACTTTTAGATTCGATGGCCACTTAACCATTGTCACAGGTGCCTGTGGTGGTTTAG 73
                                                                               TGCCCACCTTTACACTCGACGGTCATGTTGGCATCGTCACCGGTGGTGCACGTGGGTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (613) 759-1314
(613) 759-6566
                                                                                                                                             Conservative
                                                                                                                                                                                                               /dev stage="Assexual"

/lab_host="B. coli (Sure cells)"

/clone_lib="Fg02_ARFC_ECORC_Fusarium_graminearum_mycelium"

/clone_lib="Fg02_ARFC_ECORC_Fusarium_graminearum_mycelium"

/note="Wector: Bluescript SK+/XhoI-ECORI; Site_1: EcoRI;

Site_2: XhoI; Mycelial tissue was collected from V8 agar

plates after a growth period of 6-7 days at 25 C with 14

hrs (FL/UV) day ligth exposure. Mycelia was ground in

liquid nitrogen prior it's storage at -80 C until RNA

extraction. Directional cloning with 5' end of cDNA cloned

into EcoRI site of pBluescript and 3' end of cDNA cloned

into XhoI site of pBluescript (Stratagene, La Jolla, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21, Central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             harrislj@agr.gc.ca.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:5518"
/clone="Fg02_10b03"
/tissue_type="Mycelial tissue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="DAOM 180378"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Gibberella
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                                                                                                                                                           14.5%;
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                                                                                                                                            Score 118.4; DB 4;
Pred. No. 1.2e-22;
8; Mismatches 295;
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, Robert,L.S.,
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                                                                                                                                                  Department of Eukaryotic
Rockville, MD 20850, USA
Tel: 301-838-3543
Tex: 301-838-0208
                                                                                                                                                                                                                                                    Unpublished (2003)
Other_ESTs: CCAI990TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF677471
713 bp mRNA linear EST 16-AUG-2 CCAI990TF C.neoformans strain JEC21 Cryptococcus neoformans var. neoformans cDNA clone CCAI990, mRNA sequence.
                                                                                                                                                                                                                                                                                   End sequencing of clones 
JEC21 cDNA library
                                                                                                                                                                                                                                                                                                                                                                                              Cryptococcus neoformans var. neoformans
                                                                                                                                                                                                                                       Contact: Brendan Loftus
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                 var.
                                                                                                                                                                                                                                                                                                                                                                                                                               Cryptococcus neoformans var.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF677471.1 GI:41531630
                                                                                                                                                                                                                                                                                                                    Loftus, B.
                                                                                                                                                                                                                                                                                                                                                               deterobasidiomycetes;
                                                                                                                          11: crypt@tigr.org
primer: TF.
                                                                                                                                                                                                                                                                                                                                 (bases 1 to 713)
                                                                                                                                                                                                                                                                                                                                                                                                                  neoformans
              /db_xref="taxon:40410"
/clone="CCAI990"
                                                             /organism="Cryptococcus
/mol_type="mRNA"
clone_lib="C.neoformans"
                                              strain="JEC21"
                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              Basidiomycota; Hymenomycetes;
                                                                                                                                                                                                                                                                                                                                                               Tremellomycetidae;
                                                                                                                                                                                                                                                                                                  from
                                                                                                                                                                                                      Genomics,
                                                                                                                                                                                                                                                                                                                                                                                                                              neoformans
                                                                                                                                                                                                                                                                                                    þ
                                                                                                                                                                                                                                                                                                    Full length
                                                                           neoformans
strain JEC21"
                                                                                                                                                                                                      TIGR,
                                                                                                                                                                                                                                                                                                                                                                                                                            (Filobasidiella neoformans
                                                                                                                                                                                                       9712 Medical Center Drive
                                                                                                                                                                                                                                                                                                    enriched,
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EST 16-AUG-2004

normalized

Tremellaceae;

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TCTCCSGGTTACATGTTGACTGCACTCACTCAGAAGAATCTTGACGACAACCBGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATTGAT-CAAAGAAGGTATCAAGGGTGCTTCTGTTTGTTTTGATTGGTTCTATGTCTGGT
                                                                        AACCCAGGTTACATCTACGGTCCTTTGACCAAGAATGTTATCAATGGTAACGAAGA 665
                                                                                                                                                                                                                            CATTIGGCTAAGACTITGGCTTGTGAATGGGCTAAGTACAACATCAGAGTTAATTCTTTA 609
                                                                                                                                                                                                                                                                                                        TCCATTGTCAACGTTCCTCAGCCTCAGGCTCCYTATAATGCYGCCAAAGCYGGTGTGCGC
                                                                                                                                                                                                                                                                                                                                                                                    GCCATTGTCAACGATCCTCAAAACCAAGTTGTCTACAACATGTCCAAGGCTGGTGTTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGTCGAGGCTTGTTTAGCCGAGGTTGTTAAGGAGCACGGAAAGATCGACA---ACCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGTTCACAAGGTGTTTGCTCAAGTTGCTAAGGATTTTGGTAAGTTGCCATTGCACTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAAGGAAGAAGCAGAAGCAGACTAGCTTGATCATTGAAGAGTTCAAAAAAGGAGAACC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCAAGAAAAGACTGCTGCCAAACCAAGCCGAATACCACAAATA---CGCTACTGAAGAAT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAAGTTGAAAGAAGTTCCAAAGATGGGTTCATATGCCTGTGATATTTCTGATTCTGATA 250
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RESULT 5
CF701403/c
LOCUS
                                                                                                                                                    REFERENCE
AUTHORS
TITLE
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                                                                                                      JOURNAL COMMENT
                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                     CF701403 836 bp mRNA linear CCACTIATF C.neoformans strain JEC21 Cryptococcus neoformans cDNA clone CCACTI6, mRNA sequence. CF701403 CF701403.1 GI:41555562
Department of Eukaryotic
Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
                                                                                                                                                                                                                        Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales;
                                                                                                                                                                                                                                                                         var.
                                                                     TIGR
                                                                                                     Unpublished (2003)
Other_ESTs: CCACT16TR
                                                                                                                                                                                                                                                                                        Cryptococcus neoformans var.
                                                                                       Contact: Brendan Loftus
                                                                                                                                                                                                          Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACACATGGCTCGATCCCTCGCCGTCGAATGGGCTCTCAAGGGTATCCGTGTCAACGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAGAAGATGGTGAAGGTTAACTTGTTGGGTTCTTTGTATGTTTCTCAAGCCTTTGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGGIGCIGITITGTACIIGCITTCIGAAICTGCITCATACACIACIGGIGCCAGCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCGTGÁCGAGTGGCTCAACCGTÁTCCCCCATGGGTCGÁÁTGGCCGÁCCCTTCTGÁTCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCATGATTGACGGCGGTTACACTTGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACTGGTTGATGGTGGTTTCACTTCTTGG
                                                                                                                                                                                     (bases 1 to 836)
                                                                                                                                    sequencing of clones
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Pred. No. 3.5e-21;
                                                       Genomics,
                                                                                                                                                           from
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                                                                                                                                                       Full length enriched,
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RESULT 6
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Matches
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Best Local Similarity
AUTHORS
                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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Seq primer: TF.
                                                                                                                                                                CF715948 836 bp mRNA linear CCAB241TF C.neoformans strain JEC21 Cryptococcus neoformans cDNA clone CCAB241, mRNA sequence.
                                             Cryptococcus neoformans var. neoformans
Bukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales;
                                                                                                                                    CF715948.1
                                                                                       var. neoformans
                                                                                                     Cryptococcus neoformans
Loftus, B.
                             Filobasidiella.
                                           Heterobasidiomycetes;
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                                                                                                                                                                                                                                                                             TCATGATTGACGGCGGTTACACTTGCTTG
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                                                                                                                                                                                                                                                                                                                                                                      TTGGTGCTGTTTTGTACTTGCTTTCTGAATCTGCTGCTTCATACACTACTGGTGCCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="C.neoformans strain JEC21"
|note="Vector: pCMVSport6; Site 1: NotI EcoRV; The full length, normalized library was prepared from a variety conditions using RNA provided by Joseph Heitman and Jennifer Lodge"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Cryptococcus
/mol_type="mRNA"
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   CP817896 777 bp mRNA linear EST 01-EST695278 Coccidioides posadasii saprobic phase cDNA librar greater than 4kb Coccidioides posadasii cDNA clone CIBB147 mRNA sequence.
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Department of Eukaryotic
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Seq primer: TF.
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Tel: 301-838-3543
Fax: 301-838-0208
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Other_BSTs: CCAB241TR
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/note="Vector: pCWVSport6; Site 1: NotI EccRV; The full
/ength, normalized library was prepared from a variety
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"
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/mol_type="mRNA"
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/strain="JEC21"
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 777)
Gardner, M.J. and Cole, G.T.
Analysis of gene expression in Coccidioides posadasii mycelia spherules via expressed sequence tags
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
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Fax: 301 838 0208
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AGCTTACTGGTTGATGGTGGTTTCACTT 811
                                   CTCATGGGCCCAGTGACGTTCTTATTGAGTGA--
                                                                   TACATTGGTGCTGTTTTGTACTTGCTTTCTGAATCTGCTGCTTCATACACTACTGGTGCC 783
                                                                                                                                           GAATTGTACAACAGATGGATCTCTGGTATCCCACAACAAAGAATGTCCGAACCAAAGGAA
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/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii saprobic phase
library, greater than 4kb"
/note="Vector: pBxpress 1; Site_1: Not I; Site_2:
Coccidioides posadasii saprobic phase cDNA library
fractionated cDNA > 4 kb"
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/strain="C735"
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/clone="CIBB147"
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Pred. No. 5.3e-21;
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Best Local Similarity
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1 (bases 1 to 787)

Gardner, M.J. and Cole, G.T.

Analysis of gene expression in Coccidioides posadasii mycelia and Analysis of gene expression to Coccidioides posadasii mycelia and Expression sequence tags
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Tel: 301 838 3519
Fax: 301 838 0208
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The Institute for Genomic Research
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CF824542.1 GI:45930599
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                                                                                                         GTTATCCATTTGGCTAAGACTTTGGCTTGTGAATGGGCTAAGTACAACATCAGAGTTAAT 603
                                                                                                                                                                                                                            GCCAAACATCTGAT---GGCTCGCAAGTCGCCTGGCAGCATTGTGTTCATTGGAAGCATG
                                                                                                                                                                                                                                                                 GCTAAGCCATTGATCAAAGAAGGTATCAAGGGTGCTTCTGTTGTTTTTGATTGGTTCTATG
                                                                                                                                                                                                                                                                                                  CGCATGCAGAAACTCTGGTCCGTCAACGTTGATGGGTCATATCTTTTTGCAGTTGCTGTT
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                                                                        ATAAGGCACTTGGCTGCTTCCTTGGCAGTTGAATGGGCAAGTGTGGGAATCAGAGTGAAC
                                                                                                                                                                                                                                                                                                                                                                              CATCTGGTCACATCTGCGGGGTTCACTGAAAACTTTGACGCCGTGTCCTACCCGCATGAT
                                 TCTTTAAACCCAGGTTACATCTACGGTCCTTTGACCAAGAATGTTATCAATGGTAACGAA 663
                                                                                                                                                  TCTGGTGCCATTGTTAACGTGCCTCAGCCACAAGCGCCGTACAATGCTGCAAAGGCTGCG
                                                                                                                                                                                     TCTGGTGCCATTGTCAACGATCCTCAAAACCAAGTTGTCTACAACATGTCCAAGGCTGGT
 TGTATCAGTCCAGGATACATGTTGACTGCCCTGACCCGCAAGATTCTTGACGACAACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV; Coccidioides posadasii saprobic phase cDNA library, size fractionated cDNA 2 to 4 kb" ^{\circ}
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="saprobic phase (mycelia)"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii saprobic phase cDNA
/lbrary, 2 to 4 kb"
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/clone="CIDAR90"
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Pred. No. 5.3e-21;
0; Mismatches 227;
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                                                                                                                                                                                                                                                                                             274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockvil
Tel: 301 838 3519
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Onygenales; mitosporic Onygenales; Coccidioi 1 (bases 1 to 738)
Gardner,M.J. and Cole,G.T.
Analysis of gene expression in Coccidioides spherules via expressed sequence tags
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Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
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EST689764 Coccidioides posadasii saprobic phase cDNA library,
greater than 4kb Coccidioides posadasii cDNA clone CIBA394 3' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2003)
Other_ESTs: EST689765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: gardner@tigr.org.
Location/Qualifiers
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                   TCTGGTGCCATTGTCAACGATCCTCAAAAACCAAGTTGTCTACAACATGTCCAAGGCTGGT 543
                                                                                                                                                                                                                                         CACTTGGTTAACACAGCTGGTTACTGTGAAAACTTCCCATGTGAAGATTACCCAGCCAAG 363
                                                                                                        GCTAAGCCATTGATCAAAGAAGGTATCAAGGGTGCTTCTGTTTTTGATTGGTTCTATG
                                                                                                                                              CGCATGCAGAAACTCTGGTCCGTCAACGTTGATGGGTCATATCTTTTTGCAGTTGCTGTT
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                                                                                                                                                                                                                      CATCTGGTCACATCTGCGGGGTTCACTGAAAACTTTGACGCCGTGTCCTACCCGCATGAT
TCTGGTGCCATTGTTAACGTGCCTCAGCCACAAGCGCCGTACAATGCTGCAAAGGTTGCG
                                                                      GCCAAACATCTGAT---GGCTCGCAAGTCGCCTGGCAGCATTGTGTTCATTGGAAGCATG
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                                                                                                                                                                                                                                                                                                                                                                                  /dev stage="saprobic phase (mycelia)"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone lib="Coccidioides posadasii saprobic phase cDNA
library, greater than 4kb"
/note="Vector: pExpress 1, Site 1: Not I; Site 2: Eco RV,
Coccidioides posadasii saprobic phase cDNA library, size
fractionated cDNA > 4 kb"
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/mol_type="mRNA"
/strain="C735"
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clone="CIBA394"
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Pred. No. 1.5e-20;
0; Mismatches 228
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524 ACAACATGTCCAAGGCTGGTGTTATCCATTTGGCTAAGACTTTGGCTTGTGAATGGGCTA
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676 bp mRNA linear EST 01-AFF
EST701925 Coccidioides posadasii saprobic phase cDNA library,
4 kb Coccidioides posadasii cDNA clone CIDAR90 5' end, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                   The Institute for Genomic Research 9712 Medical Center Drive, Rockville, Tel: 301 838 3519
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gardner, M.J. and Cole, G.T.
Analysis of gene expression in Coccidioides posadasii spherules via expressed sequence tags
Unpublished (2003)
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1 (bases 1 to 676)
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                                TTGTGTTCATTGGAAGCATGTCTGGTGCCATTGTTAACGTGCCTCAGCCACAAGCGCCGT
                                                             TIGITITGATIGGITCTATGICIGGIGCCATIGICAACGATCCICAAAACCAAGIIGICI
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                                                                                                                                                                                                                                                                                                                                                                                      il: gardner@tigr.org
primer: M13 Reverse
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gardner MJ
                                                                                                                                                                     library, 2 to 4 kb"

/note="Vector: pExpress 1; Site 1: Not 1; Site 2: Eco
Coccidioides posadasii saprobic phase cDNA library, si
fractionated cDNA 2 to 4 kb"
                                                                                                                                                                                                                             /dev_stage="saprobic phase (mycelia)"
/lab_host="E coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii saprobic phase cDNA
                                                                                                                                                                                                                                                                               db_xref="taxon:199306"
clone="CIDAR90"
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Query Match
Best Local Similarity
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EST.
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Tel: +44(0)1592 763133
Fax: +44(0)1592 76981
Email: john.keon@bbsrc.ac.uk
Insert Length: 800 Std Error: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  718
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CO136295.1 GI:48885273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aspergillus flavus
Aspergillus flavus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 615)
                                                                                                                                                                          Seq primer: M13 POLYA=No.
                                                                                                                                                                                                         BACKWARD: M13R
                                                                                                                                                                                                                                                                           Email: jiuyu@srrc.ars.usda.gov
Contact Dr. Yu at USDA/ARS SRRC
                                                                                                                                                                                                                                                                                                                                                              Food and Feed Safety Research Unit
USDA/ARS, Southern Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Yu J
                                                                                                                                                                                                                                                                                                                                                                                                                Yu,J., Whitelaw,C.A., Nierman,W.C., Bhatnagar,D. and Cleveland,T.E. Aspergillus flavus expressed sequence tags for identification of genes with putative roles in aflatoxin contamination of crops FEMS Microbiol. Lett. (2004) In press
                                                                                                                                                                                                                             FORWARD: M13F
                                                                                                                                                                                                                                                                                                               Tel: 504 286 4405
Fax: 504 286 4419
                                                                                                                                                                                                                                                             information
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                                                                                                                                                                                                                                         PRimers
                                                                                                                                                                                                                                                                                                                                                Robert E. Lee Boulevard, New Orleans, LA
                                            /strain="NRRL 3357"
/db_xref="taxon:5059"
/clone="NAFBQ16"
                                                                                                                                                     Location/Qualifiers
/cell_type="mycelia"
/dev_stage="developmental
                                                                                                                 organism="Aspergillus"
                                sex="asexual mycelia"
                                                                                                  type="mRNA
                                                                                                                                                                                          Forward
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                                                                                                                                                                                                                                                        GCTAAGACTTTGGCTTGTGAATGGGCTAAGTACAACATCAGAGTTAATTCTTTAAACCCA
                                                                                                                                                                                                                                                                                                                                                        GTCAACGATCCTCAAAACCAAGTTGTCTACAACATGTCCAAGGCTGGTGTTATCCATTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCGCCGGATTCACGGAAAAACTTCGATGCCATCTCCTACCCTCACGACCGTCTGCAAAAG
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                                              AAGTGGATCTCGCTCATCCCCACCGGCAAGATGGGTACTCCCGAGGACCTGATGGGTCCC
                                                                                                                                                                                 GGTTACATCTACGGTCCTTTGACCAAGAATGTTATCAATGGTAACGAAGAATTGTACAAC
                                                                                                                                                                                                                                                                                                                     GTCAACGTGCCGCAGCCCCAGGCTCCTTACAACGCCGCCAAGGCCGCTGTTCGTCAACTT
                                                                                                                                                                                                                                                                                                                                                                                                           CTCATGGAGCGCAAGGTTCCGGGCAGCATTGTCATGATTGGTAGCATGTCTGGTGCTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGTGAAGGTTAACTTGTTGGGTTCTTTGTATGTTTCTCAAGCCCTTTGCTAAGCCATTG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAGCTGGTTACTGTGAAAACTTCCCCATGTGAAGATTACCCAGCCAAGAACGCTGAGAAG
  GITTTGTACTTGCTTTCTGA 755
                                                                                        AGATGGATCTCTGGTATCCCACAACAAAGAATGTCCGAACCAAAGGAATACATTGGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="vector: pBlueScript (SK+) (Stratagene), antibiotic selection marker: Carbenicillin; Site 1: Not!, at the 5 prime end; Site 2: EcoRI, at the 3 prime end; This normalized cDNA expression library was constructed using a mixture of mycelial cells grown under eight different medium conditions and harvested at 5 time points (18, 24, 48, 72, 96 hours). The poly-A sequence was trimmed off before ligating to vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. coli DH10B T1 resistant cell
/clone_lib="Aspergillus flavus Normalized
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Pred. No. 1.4e-17;
0; Mismatches 267;
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REFERENCE
AUTHORS
TITLE
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CO141255
LOCUS
                                                                                                                  ACCESSION
VERSION
KEYWORDS
                                                                                                      SOURCE
                                                                                                                                                                                       DEFINITION
                                                                                    ORGANISM
                                                                                                                                    Aspergillus
CO141255
CO141255.1
                                                                               Aspergillus flavus
Aspergillus flavus
                                                                                                                                                                     CO141255

447 bp mRNA linear EST 17-UUN-
EST835926 Aspergillus flavus Normalized cDNA Expression Library
Aspergillus flavus cDNA clone NAFEA37 5' end, mRNA sequence.
 Yu,J., White Aspergillus
                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
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 Whitelaw, C.A., Nierman, W.C.,
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572

GTTACCTTCCTGCTCAGTGA

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Best Local Similarity
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AU249728
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FEMS Microbiol
Contact: Yu J
    AU249728.1 GI:4650
EST.
Lolium multiflorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq prime POLYA=No.
                                                                                AU249728
                                                                                             AU249728
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BACKWARD: M13R
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1100 Robert E. Lee Boulevard, New Orleans, 1
Tel: 504 286 4405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: jiuyu@srrc.ars.usda.
Contact Dr. Yu at USDA/ARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR PRimers
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Fax: 504 286 4419
                                                                                                                                                                                                GAATGTCCGAACCAAAGGAATACATTGGTGCTGTTTTGTACTTGCT 749
                                                                                                                                                                                                                                                                                        GTCACGACATCCGGGTGAACTGCATCAGCCCTGGATACATGCTTACTGCCCTGACCCGCA
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                                                                                                                                                                     AGATGGGTACTCCCGAGGACCTGATGGGTCCCGTTACCTTCCTGCT 447
                                                                                                                                                                                                                                                                                                                                                                                                            TIGTCATGATTGGTAGCATGTCTGGTGCTATCGTCAACGTGCCGCAGGCCCCAGGCTCCTT
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                                                                               511 bp
SL Lolium multiflorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /notes vector: pBlueScript (SK+) (Stratagene), antibiotic selection marker: Carbenicillin; Site 1: Not; at the 5 prime end; Site 2: EcoRI, at the 3 prime end; This normalized cDNA expression library was constructed using mixture of mycelial cells grown under eight different medium conditions and harvested at 5 time points (18, 24, 48, 72, 96 hours). The poly-A sequence was trimmed off
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="developmental stages from 18 to 96 hours"
/lab_host="E. coli DH10B T1 resistant cells"
/clone_lb="Aspergillus flavus Normalized cDNA Expres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Aspergillus
/mol_type="mRNA"
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siol. Lett. (2004) In press
                                     GI:46506997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.9%;
58.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 97.2; DB 7;
Pred. No. 1.4e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .gov
SRRC (jiuyu@srrc.ars.usda.gov)
      ryegrass)
                                                                                CDNA
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                                                                             clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
Watson,R.J., Heys,R., Couroux,P., De Hattori,J., Lacroix,C., Masotti,M., O Singh,J.A., Sprott,D. and Tinker,N.A.
                                                Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomy
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 892)
                                                                                                         EST.
Gibberella
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                                            (bases 1 to 892)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CN811863 892 bp mRNA linear EST 01-JUN-200-
FG09_08p20 A FG09_AAFC_ECORC_Fusarium_graminearum_simple_substrate
Gibberella_zeae cDNA clone FG09_08p20, mRNA sequence.
CN811863
CN811863.1 GI:47835874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: sikeda67@jfsass.or.jp
contact:Tadashi Takamizo (takamizo@affrc.go.jj
National Institute of Livestock and Grassland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Japan Grassland Farming Forage Seed Association(JFSA)
Forage Crop Research Institute(FCRI)
Higasiakada 388-5, Nishinasuno, Tochigi 329-2742, Jap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 81-287-37-6755
Fax: 81-287-37-6757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
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/tissue_type="Powdery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Lolium multiflorum"
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Pred. No. 2.1e-15;
D; Mismatches 138;
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yta; Liliopsida; Poales; Poaceae;
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De Moors, A., Harris, L.J., ., Ouellet, T., Robert, L.S.,

Sordariomycetes;

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Best Local Similarity 54.5
Matches 204; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A cDNA library prepared from Fusarium graminearum grown on a simple substrate Unpublished (2003) Contact: Watson, Robert.J. Eastern Cereal and Oilseed Research Centre Agriculture and Agri-food Canada Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: watsonrj@agr.gc.ca.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (613) 759-1655
Fax: (613) 759-1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAAAGAAGGTATCAAGGGTGCTTCTGTTGTTTTGATTGGTTCTATGTCTGGTGCCATTG
                                                                                                                                                                                                           CCTGGACATCCCTCATTCCTCAGGGTCGCATGGGACTGCCTCAAGATTTGATGGGACCCG
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                                                                                                                                                                                                                                                                                                          GTTACATCTACGGTCCTTTGACCAAGAATGTTATCAATGGTAACGAAGAATTGTACAACA 676
                                                                                                                                                                                                                                                                                                                                                    CTGCTTCTCTTGCAGTGGAGTGGGCTCACGCTGGAATCCGTGTCAACTGCATCTCTCCTG
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                                                                     ATGGAGGATACACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBluescript II+; Site_1: EcoRI; Site_2: XhoI; Fusarium graminearum grown on a simple substrate-minimal media supplemented with amino acids."
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/mol_type="mRNA"
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Pred. No. 1.2e-14;
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ABJ26225 ABJ2525181 ADG25185 ADS42929 ADS242929 ADS25559 ADS25559 ADS25559 ADS25559 ADS25559 ADS2556473 ABJ25625 ADS25184 ADG25184 ADG25184

Abj26225 Adg25179 Adg25185 Adg25189 Adg25189 Adg25185 Adg25184 Adg25184 Abj266473 Abj26473 Abj26747 Adg25184 Abj25184 Adg25184 Adg25184

7 A. altern
1 Bacterial
2 Klebsiell
3 Klebsiell
5 Aspergill
7 Bacterial
7 Staphyloc
7 Staphyloc
8 Staphyloc
9 Staphyloc

Bacterial Bacterial Bacterial

70 788

778586

ALIGNMENTS

Bacterial
C. fulvum
C. fulvum
Bacterial

Bacterial Bacterial

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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: geneseqp1990s:*
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4: geneseqp2001s:*
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Gapop 10.0 , Gapext 0.5
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| Sequence 272 AA; | L-xylulose reduct | is an Ambrosiozyma monospora N | in producing fermentation products or in conversion of cheap biomass to | The present invention relates to a NADH dependent L-xylulose reductase | 1 | Claim 26; SEO ID NO 2: 15pp; English. | מפברתו בירימונים. | producing termentation products or in conversion of cheap blomass to | reductase, use | N-PSUB; ADQ94601. | WPI; 2004-517001/49. | Verho R, Richard P, Penttila M; | | (VALW) VALTION TEKNILLINEN TUTKIMUSKESKUS. | | | | | 16-FEB-2001; 2001FI-00000308. | | 24-NOV-2003: 2003US-00720018. | | 08-JUL-2004. | | US2004132074-A1. | | Ambrosiozyma monospora. | | | NADH dependent L-xylulose reductase; fermentation; biomass; enzyme; | 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | Ambrosiozyma monospora NADH dependent L-xylulose reductase. | | 23-SEP-2004 (first entry) | STATE OF STA | 2004603 | ADQ94602 standard; protein; 272 AA. | | if 1 |

Result No.

Score

Match

Length

DB

IJ

Ads24003 Aae28702 Adj98100 Adj98118

Bacterial
Bacterial
Trichoder
Trichoder
Ketoreduc
Ketoreduc
Ketoreduc
C. magnol
Amino aci
Ketoreduc
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Ketoreduc
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Ketoreduc

Adq94602 Aay56815 Adn20270

Ambrosioz Bacillus

Description

SUMMARIES

ADQ94602
AAY56215
ADM20270
ADM

Ady 98098
AAW64777
Aag63579
Adj98066
Adj98060
Adj98060
Adj98104
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Query Match

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                                                                                            Matches
                                                                                                                                          Query Match
                                                                                                                                                                                      Sequence 258 AA;
                                                                                                                                                                                                                                    The invention relates to gene encoding D-arabinitol dehydrogenase, isolated from Bacillus sp. IKD-5A868 strain. The protein can be expressed by standard recombinant methodologies. D-arabinitol dehydrogenase is used as a clinical diagnosing agent for mycosis. The present sequence represents the D-arabinitol dehydrogenase enzyme
                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabinitol dehydrogenase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-1998;
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                                                                                                                       Local
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)B; AAZ46762, A
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                                                                                                                                                                                                                                                                                                                                                                               Page 10-11; 14pp; Japanese.
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                                              FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDI--DQEKTAAKQAEYHKYATEELK
  FRLDGRVTIVTGAGMGLGRAMALALAQAGSHIVIADIRADEAQEAA
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                                                                                                                                        Score
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; Mismatches 0;
                                                                                            Pred. No. 5.16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           ng agent f
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1. No. 5.1e-35;
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KW Cold
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IS-1-1
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promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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(SLAT/)
(CHEN/)
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                                                                                                                                                                                                                                                                                                      The invention relates to a recombinant DNA promoter functional in a plant cell, where
                                                                                                                                                                                                                                                                                                                                                                                               Claim
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SLATER S
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GOLDMAN
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polypeptide.
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heat tolerance; drought tolerance; herbicide;
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ARSSULT 4
ARSSULT 4
ARSS2102
ADS23
XX
ADS2403
AC ADS2
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AC ADS2
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Bact
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Recc
KW Colc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                             18-DEC-2003.
                                                                                                                                                                                                                                                                                                                                                                   US2003233675-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacterial polypeptide #13036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS24003 standard; protein; 211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress
      (CHEN/)
                                                               (HINK/)
                                                                                                                                                                                     21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                              20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADS24003
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                                                                                                                           (CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 KNAEKMVKVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKA
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HINKLE G J.
SLATER S C.
CHEN X.
GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
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                                                                                                                               CAO Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDDLIGAAIFLAS-PASDYMTGHDLVIDGGYTVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKWKKVIDVNLVG-VFLSAKAEFHAMKER-KYGKIINIASMSGHIVNKPOKOTAYNASKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKEYIGAVLYLLSESAASYTTGASLLVDGGFTSW 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVIHLTRSLAAEWAPYGIRVNSISPGYIRTPLIESPNV----KDLVPLWLDMIPLGRLGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVPKMGS----YACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAG---YCENFPCEDYPA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphorus; photosynthesis;
polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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Pred. No. 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lignin; galactomannan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .7e-33;
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Matches Query Match

88;

Conservative

38;

Local

Similarity

28.0%;

Score 396; DB 8; Pred. No. 3.4e-32; Mismatches

Length 211; Indels

24;

4

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The invention relates to a recombinant DNA construct comprising a CC promoter functional in a plant cell, where the promoter is positioned to CC provide for expression of a polynucleotide encoding a polypeptide from a CC microbial source. The invention also relates to a transformed plant CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC recombinant DNA construct and growing the transformed plant with the CC polynucleotide or polypeptide is useful for improving plant properties. CC The recombinant DNA construct is useful for producing plant properties. CC improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of CC content, improved yield by modification of protesynthesis or by phosphorus use and/or uptake, by modification of protesynthesis or by providing improved plant growth and development under at least one stress CC condition, improved lignin production or improved galactomannan CC production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part form interpresent a patent of the printed specification but was obtained in electronic condition.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              microbial source, useful for producing
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                                             Format from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲,
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211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 13036; 122pp;
                                             at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Slater SC,
                                           seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goldman
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S 밁 S 밁 Ś 밁 8 198 138 SQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAGVIHLAKTLACEWAKYN 197 60 78 μ. GVPEDLMGAVTFLLSD-ASKYITGADLRVDGGYT SEPKEYIGAVLYLLSESAASYTTGASLLVDGGFT DISDSDTVHKVFAQVAKDFGKLPLHLVNTAGYCENFPCEDYPAKNAEKWVKVNLLGSLYV 137 IRVNCISPGYMLTALXVPESLQNSXARTICXFVATRTRKILDENPELRDKWISLIPTGKM 178 IRVNSLNPGYIYGPL---------TKNVINGNEELYNRWISGIPQQRM 236 ATGVAKHLMERKAPG-SIVMIGSMSGAIVNVPQPQAPYNAAKAAVRHLASSFAVEWAGHG 118 DVSNPDSVNNALSEVIAKHGKID-HLVTSAGFTENFDAISYPYDRMQKLWGVNVDGTYLF 211 270 64; Gaps 59

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RESULT 5
AAE28702
                                                                            AAE28702;
 Trichoderma
                               29-AUG-2003
27-DEC-2002
                                                                                                     AAE28702 standard; protein; 266 AA
reesei L-xylulose reductase.
                              (revised)
(first entry)
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SAN SECTION OF SECTION Genetically modified fungus; L-arabinose; L-arabinitol 4-dehydrogenase; EC 1.1.1.12; L-xylulose reductase; EC 1.1.1.10; agricultural product; biomass; lactic acid; xylitol; forestry product; fermentable sugar;

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RESULT 6
ADJ98100
ADJ9 XX
AC ADJ9
XX
DT 06-M
XX
DE Keto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ability to utilise L-arabinose, where the fungus has been transformed with a DNA sequence encoding an L-arabinito 4-dehydrogenase (EC 1.1.1.10) or L-xylulose reductase (EC 1.1.1.10) or both the DNA sequences. Genetically modified fungus is useful for producing useful products from biomass containing L-arabinose. The useful product include ethanol, lactic acid or xylitol preferably ethanol. It is also useful to ferment a carbon source such as blomass comprising agricultural or forestry products and waste products containing L-arabinose and also other pentoses or other fermentable sugars. The present sequence is T. reesei L-xylulose reductase. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetically modified fungus for producing useful products such as ethanol, lactic acid and xylicol, from biomass containing L-arabinose,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-FEB-2001; 2001FI-00000308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ethanol; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Londesborough J,
Ketoreductase (KRED) protein SEQ ID NO:42.
                                 06-MAY-2004
                                                                                                 ADJ98100 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 3; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                has increased ability to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to genetically modified fungus with an increased lity to utilise L-arabinose, where the fungus has been transformed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                            QVVYNMSKAGVIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGI
                                                                                                                                                                                                                                                                                                            NFPCEDYPAKNAEKWVKVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQN 171
                                                                                                                                                                                                                                                                                                                                                                          KNA-----EELTKEYGVKVKVYKVNQSDYNDVERFVNQVVSDFGKIDAFIAN-AGATA 112
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                                                                                                                                                                                                            POORMSEPKEYIGAVLYLLSESAASYTTGASLLVDGGFTS
                                                                                                                                                                                                                                              OTSYNVAKAGCIHLARSLANEWRDF-ARVNSISPGYIDTGLSDFIDEKTQEL--
                                                                                                                                                                                PMGRNGDAKELKGAYVYLVSD-ASSYTTGADIVIDGGYTT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                 (first entry)
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                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  utilize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 393; DB 5; Length 26
Pred. No. 9.9e-32;
1; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L-arabinose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 266;
                                                                                                                                                                                                                 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                 231
                                                                                                                                                                                                                                                                                                               170
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The present invention describes a method (M1) for producing 4-cyano-3-CC hydroxybutyric acid ester (I) from a 4-halo-3-hydroxybutyric acid ester (II) or 4-halo-3-ketobutyric acid ester (III), comprising providing (II) CC (III), and contacting (II) with a halohydrin dehalogenase and cyanide cunder conditions sufficient to form a reaction mixture for converting (II) to (I). Also described: (1) producing (M2) a 4-nucleophile comprising; (a) providing (II), (III) or amide; and (b) contacting (II) or amide for converting (II) or amide with a halohydrin dehalogenase and a nucleophile under conditions suitable to form a reaction mixture for converting (II) or amide to a 4-nucleophile substituted-3-hydroxybutyric acid or amide; or (c) contacting (III) or amide with a ketoreductase, a cofactor, a cc confortor regeneration system, a nucleophile and a halohydrin dehalogenase to form a reaction mixture for converting (III) or amide; and (2) a cc composition (IV) comprising halohydrin dehalogenase, a nucleophile, and (I) or amide. (M1) is useful for producing a 4-cyano-3-hydroxybutyric acid ester from a 4-halo-3-hydroxybutyric acid ester or 4-halo-3-c ketobutyric acid ester. (M2) is useful for producing a 4-nucleophile substituted-3-hydroxybutyric acid ester or 4-halo-3-c ketobutyric acid ester. (M2) is useful for producing a 4-nucleophile substituted-3-hydroxybutyric acid ester or 4-halo-3-c ketobutyric acid ester. (M2) is useful for producing a 4-nucleophile substituted 3-hydroxybutyric acid ester or 4-halo-3-c ketobutyric acid ester or 5-hydroxybutyric acid ester or 5-hydroxybutyric acid ester or 6-halo-3-bydroxybutyric acid ester or 6-halo-3-bydroxybutyric acid ester or 6-halo-3-c ketobutyric acid ester or 6-halo-3-bydroxybutyric acid ester or 6-halo-3-bydroxybutyric acid ester or 6-halo-3-bydroxybutyric acid ester or 6-halo-3-bydroxybutyric acid ester 6-halo-3-bydroxybutyric acid ester 6-halo-3-bydroxybutyric acid ester 7-halo-3-c 6-halo-3-bydroxybutyric acid ester 8-halo-3-bydroxybutyric acid ester 9-halo-3-hydroxybut
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                                                                                                                                                                                         Matches
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4-nucleophile substituted-3-hydroxybutyric acid amide;
4-substituted 3-hydroxybutyric acid derivative; KRED; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4-cyano-3-hydroxybutyric acid ester; 4-halo-3-hydroxybutyric acid ester; 4-halo-3-ketobutyric acid ester; halohydrin dehalogenase; cyanide; 4-mucleophile substituted 3-hydroxybutyric acid ester; amide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2002; 2002US-0402436P.
11-AUG-2003; 2003US-00402436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004015132-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing 4-cyano-3-hydroxybutyric acid ester from 4-halo-3-hydroxybutyric acid ester, comprises contacting 4-halo-3-hydroxybutyric acid ester with halohydrin dehalogenase and cyanide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADJ98099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-238752/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-AUG-2003; 2003WO-US025263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 9; SEQ ID NO 42; 168pp; English.
                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CODE-) CODEXIS INC
                                                                                                                                                                                                               Local
                                                                                                 29
                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                      283
---KVKAYKANVSSSDAVKQTIEQQIKDFGHLDIVVAN-AGIPWTKGAYIDQDDDKHFDQ
                                         EVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAG--YCENFPCEDYPAKNAEK 125
                                                                                               FKLNGKVASITGSSSGIGYALAEAFAQVGADVAIWYNSQDATGKAEALAKKYGV-----
                                                                                                                                           FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grate JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sheldon R,
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                               26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gray DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang LA;
                                                                                                                                                                                            52;
                                                                                                                                                                                       Score 381; DB 8;
Pred. No. 1.9e-30;
2; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gruber JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huisman
                                                                                                                                                                                                                                        Length 283;
                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Мa
                                                                                                                                                                                              22;
                                                                                                                                                                                              Gaps
         138
                                                                                                                                                       67
                                                                                                      82
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MVKVNLLGSLYVS----QAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAG 181

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RBSULT 7

ADJ98118

ID ADJ9

XX ADJ9

XX ADJ9

XX ADJ9

XX ADJ9

XX ACT

DX Ketc

XX 4-cy

XX A-nc

XX
           CC (III) or 4-halo-3-ketobutyric acid ester (III), comprising providing (II) conditions sufficient to form a reaction mixture for converting (II) to (I). Also described: (I) producing (M2) a 4-nucleophile comprising: (a) providing (II) (III) or amide from (II) or amide, comprising: (a) providing (II), (III) or amide from (II) or amide, comprising: (a) providing (II), (III) or amide from (II) or amide, comprising: (a) providing (II), (III) or amide from (II) or amide, conditions suitable to form a reaction mixture for converting (II) or amide to a 4-nucleophile substituted-3-hydroxybutyric acid or amide; or (c) contacting (III) or amide with a ketoreductase, a cofactor, a cofactor regeneration system, a nucleophile and a halohydrin dehalogenase to form a reaction mixture for converting (III) or amide to form a reaction mixture for converting (III) or amide to a 4-composition (IV) comprising halohydrin dehalogenase and a mucleophile, and (2) a composition (IV) comprising halohydrin dehalogenase a nucleophile, and (I) or amide. (M1) is useful for producing a 4-cyano-3-hydroxybutyric acid ester from a 4-halo-3-hydroxybutyric acid ester or 4-halo-3-composition (IV) comprising halohydrin dehalogenase and a destar from a 4-halo-3-hydroxybutyric acid ester or 4-halo-3-composition (IV) comprising halohydrin dehalogenase and (I) acid ester from a 4-halo-3-hydroxybutyric acid ester or 4-halo-3-composition (IV) comprising halohydrin dehalogenase and 4-nucleophile substituted-3-hydroxybutyric acid ester or 4-halo-3-composition (IV) comprising halohydrin dehalogenase and 4-nucleophile substituted-3-hydroxybutyric acid ester or 4-halo-3-composition (IV) composition (IV) composition (IV) composition dehalogenase composition (IV) composition (IV) composition dehalogenase compositi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method (M1) for producing 4-cyano-3-hydroxybutyric acid ester (I) from a 4-halo-3-hydroxybutyric acid este
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing 4-cyano-3-hydroxybutyric acid ester from 4-halo-3-hydroxybutyric acid ester, comprises contacting 4-halo-3-hyd acid ester with halohydrin dehalogenase and cyanide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing
ketobutyric acid ester. (M2) is u
substituted-3-hydroxybutyric acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Davis SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2002;
11-AUG-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-AUG-2003; 2003WO-US025263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4-halo-3-ketobutyric acid ester; halohydrin dehalogenase; cyanide; 4-nucleophile substituted 3-hydroxybutyric acid ester; amide; ketoreductase; cofactor; cofactor regeneration system; nucleophile; 4-nucleophile substituted-3-hydroxybutyric acid amide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4-cyano-3-hydroxybutyric acid ester; 4-halo-3-hydroxybutyric acid ester;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ketoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CODE-) CODEXIS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2004-238752/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ፷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ98117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVGAYLFLASD-AGSYATGTDIIVDGGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YIGAVLYLLSESAASYTTGASLLVDGGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRHPAKSLAVEFAPF-ARVNSVSPGYINTEISDFV---PQETQNKWWSLVPLGRGGETAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIDVDLKGVGYVAKHAGRHYRERFEKEGIKGA-LIFTASVSGHIVNIPQFQATYNAAKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grate JH,
Sheldon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002US-0402436P
2003US-00402436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KRED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₽,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gray DR, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gruber
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   ester
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO:60
for producing a r or amide. (M1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huisman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4-halo-3-hydroxybutyric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            æ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ma
   (M2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
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RESULT 8
ADJ98098
ID 98098
XX ADJ9
XX ADJ9
XX ADJ9
XX ACY
XX Y-CY
XX 4-CY
XX W4-NU
XX W4-NU
XX Synt
XX W020
XX Synt
XX W020
XX I1-A
XX I1-A
XX I1-A
XX I1-A
XX ICOD
XX II-A
XX ICOD
XX II-A
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                                                                           Producing 4-cyano-3-hydroxybutyric acid ester from 4-halo-3-hydroxybutyric acid ester, comprises contacting 4-halo-3-hyd acid ester with halohydrin dehalogenase and cyanide.
                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2002;
11-AUG-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ketoreductase; cofactor; cofactor regeneration system; nucleophile;
4-nucleophile substituted-3-hydroxybutyric acid amide;
4-substituted 3-hydroxybutyric acid derivative; KRED; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4-cyano-3-hydroxybutyric acid ester; 4-halo-3-hydroxybutyric
4-halo-3-ketobutyric acid ester; halohydrin dehalogenase; cya
4-nucleophile substituted 3-hydroxybutyric acid ester; amide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for producing 4-substituted 3-hydroxybutyric acid derivatives. present sequence represents a ketoreductase (KRED), which is used in texemplification of the present invention.
                                                                                                                                                                                  WPI; 2004-238752/22.
N-PSDB; ADJ98097.
                                                                                                                                                                                                                                                             Newman
                                                                                                                                                                                                                                                                                        Davis SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-AUG-2003; 2003WO-US025263
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Sheldon
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2003US-00402436.
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                                                                                                                                                                                                                                                                                   Gray
                                                                                                                                                                                                                                                             Wang
                                                                                                                                                                                                                                                                                        DR,
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Pred.
                                                                                                                                                                                                                                                                                        Gruber JM,
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No. 1.9e-30;
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                                                                                                                                                                                                                                                                                        Huisman
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                                                                                                   4-halo-3-hydroxybutyric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for producing 4-substituted 3-hydroxybutyric acid d present sequence represents a ketoreductase (KRED), which exemplification of the present invention.
                                01-SEP-1997;
                                                                                                                                                                                                                    Candida magnoliae.
                                                                                                                                                                                                                                                                                  ethyl 4-chloroacetoacetate
                                                                                                                                                                                                                                                                                                                   Carbonyl reductase; ethyl (S)-4-chloro-3-hydroxybutanoate production; optically active 3-hydroxybutanoate ester production;
                                                                                                                                                                                                                                                                                                                                                                                                               C. magnoliae carbonyl reductase
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                                                                                              13-AUG-1998.
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; Pred. No. 2.4e-30;
49; Mismatches 99
                                                                                                                                                                                                                                                                                         conversion.
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h is used in the
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RESULT 10
AAG63579
ID AAG63579
ID AAG63
XX AAG63
AC AAG63
AC AAG63
AC AAG63
XX IS-OC
XX Methi
KW Methi
KW MADPH
XX NADPH
XX WO20C
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Best Local Similarity
Matches 99; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -chloro-3-hydroxybutanoate using NADPH as a coenzyme, but is not significantly active on ethyl acetoacetate. It has working pH 5.5 to and working temperature 50-55 degrees C. It is stable for at least 30 minutes at 40 degrees C at pH 7. It is inhibited by mercury ions and quercetin and has a molecular weight of 76 kDa by gel filtration and kDa by SDS-PAGE. The protein can be used to provide for sufficient production of optically active 3-hydroxybutanoate esters for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carbonyl reductase derived -halo-acetoacetate ester(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yasohara Y,
Yamamoto K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-1997;
30-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Fig 1; 60pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is the Candida magnoliae carbonyl reductase of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KANF ) KANEKA CORP
                                                                                             directed evolution;
NADPH-dependent carl
                                                                                                                                                                                                                                                     AAG63579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synthetic intermediates for pharmaceuticals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention.
                                                                                                                            Methionine gamma-lyase; mdeA gene; free
                                                                                                                                                           Amino acid
                                                                                                                                                                                         15-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            halo-acetoacetate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1998-447222/38
                                                                                                                                                                                                                                                                                                                                                                                             198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 MVKVNILGSLYVS----QAFAKPLIKEGIKGASVVLIGSMSGAIVNDÞQNQVVYNMSKAG 181
                                                                                                                                                                                                                                                                                                                                                              242 YIGAVLYLLSESAASYTTGASLLVDGGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 ---KVKAYKANVSSSDAVKQTIEQQIKDFGHLDIVVAN-AGIPWTKGAYIDQDDDKHFDQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVDVDLKGVGYVAKHAGRHFRERFEKEGKKGA-LVFTASMSGHIVNVPQFQATYNAAKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVPKMGSYACDISDSPTVHKVFAQVAKDFGKLPLHLVNTAG--YCENFPCEDYPAKNAEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FKLNGKVASITGSSSGIGYALAEAFAQVGADVAIWYNSHDATGKAEALAKKYGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK
                                                                                                                                                                                                                                                    standard; protein; 283
                                                                                                                                                                                                                                                                                                                                 LVGAYLFLASD-AGSYATGTDIIVDGGYT
                                                                                                                                                                                                                                                                                                                                                                                                                            VIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPKE
                                                                                                                                                                                                                                                                                                                                                                                               VRHFAKSLAVEFAPF-ARVNSVSPGYINTEISDFV---PQETQNKWWSLVPLGRGGETAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The protein converts ethy
                                                                                                                                                         sequence of a NADPH-dependent carbonyl reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kizaki N,
Kawabata 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                         (first entry)
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                                                                                               carbonyl reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.7%;
                                                                                                               molecular breeding;
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, Kita K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from Candida magnoliae - selectively reduces 4
to (S)-4-halo-3-hydroxy-butanoate ester(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 378; DB 2;
Pred. No. 3.9e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wada M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4-chloroacetoacetate to ethyl (S)-4
                                                                                                                                                                                                                                                                                                                                   281
                                                                                                                                                                                                                                                                                                                                                                 270
                                                                                                                              folding energy; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100;
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                                                                                                                                 shuffling;
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WO200155342-A2 Candida magnoliae

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RESULT 11
ADJ98066
ID ADJ98
XX
AC ADJ98
XX
DT 06-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a NADPH-dependent carbonyl reductase. The CC polynucleotide was modified using using the method of the invention. The specification describes a method for designing a synthetic complex the predicted. The method comprises providing a starting polynucleotide, comprises provided by replacing a codon with a cC different codon to provide a modified polynucleotide, determining free cerry of folding per base of the modified polynucleotide, determining free cerry of folding per base of the modified polynucleotide, and comparing this with that of the original polynucleotide. The method is useful for CC developing nucleic acid sequences that enhance expression of the encoded crotein in a heterologous host. The design and preparation of the control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                            06-MAY-2004
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                                                                         ADJ98066;
                                                                                                                    ADJ98066 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 283
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08-DEC-2000;
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DB; AAH74597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 such as methionine gamma-lyase from P. putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99,
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                                                                                                                                                                                                                                 LVGAYLFLASD-AGSYATGTDIIVDGGYT
                                                                                                                                                                                                                                                                         YIGAVLYLLSESAASYTTGASLLVDGGFT 270
                                                                                                                                                                                                                                                                                                                                                                   VIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MVKVNLLGSLYVS----QAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAG---YCENPPCEDYPAKNAEK 125
                                                                                                                                                                                                                                                                                                                      VRHFAKSLAVEFAPF-ARVNSVSPGYINTEISDFV---PQETQNKWWSLVPLGRGGETAE
                                                                                                                                                                                                                                                                                                                                                                                                                VVDVDLKGVGYVAKHAGRHFRERFEKEGKKGA-LVFTASMSGHIVNVPQFQATYNAAKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---KVKAYKANVSSSDAVKQTIEQQIKDFGHLDIVVAN-AGIPWTKGAYIDQDDDKHFDQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FKLNGKVASITGSSSGIGYALAEAFAQVGADVAIWYNSHDATGKAEALAKKYGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRFDGHLTIVTGACGGLABALIKGLLAYGSDIALLDIDQBKTAAKQABYHKYATEBLKLK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                            (first entry)
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2000US-00734237.
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                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.7%;
36.8%;
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                                                                                                                    283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid sequences for improved amplification, comparing free energy of folding of a a modified polynucleotide having a codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 378; DB 4;
Pred. No. 3.9e-30;
18; Mismatches 100
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                                                                                                                                                                                                                                 281
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                                                                                                                                                                                                                                                                                   (c) contacting (III) or amide with a ketoreductase, a cofactor, a cofactor regeneration system, a nucleophile and a halohydrin dehalogenase to form a reaction mixture for converting (III) or amide to a 4-composition (IV) comprising halohydrin dehalogenase, a nucleophile, and (2) a composition (IV) comprising halohydrin dehalogenase, a nucleophile, and (I) or amide. (M1) is useful for producing a 4-cyano-3-hydroxybutyric acid ester or 4-halo-3-kydroxybutyric acid ester or amide. (M1) and (M2) are useful for producing 4-substituted 3-hydroxybutyric acid derivatives. The present sequence represents a ketoreductase (KRED), which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  under conditions sufficient to form a reaction mixture for converting (II) to (I). Also described: (1) producing (M2) a 4-nucleophile substituted 3-hydroxybutyric acid ester or amide from (II) or amide, comprising: (a) providing (II), (III) or amide; and (b) contacting (II) or amide with a halohydrin dehalogenase and a nucleophile under conditions suitable to form a reaction mixture for converting (II) or amide to a 4-nucleophile substituted-3-hydroxybutyric acid or amide; or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Davis SC,
Newman LM,
                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method (MI) for producing 4-cyano-3-hydroxybutyric acid ester (I) from a 4-halo-3-hydroxybutyric acid ester (II) or 4-halo-3-ketobutyric acid ester (III), comprising providing (II) or (III), and contacting (II) with a halohydrin dehalogenase and cyanide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing 4-cyano-3-hydroxybutyric acid ester from 4-halo-3-hydroxybutyric acid ester, comprises contacting 4-halo-3-hyd acid ester with halohydrin dehalogenase and cyanide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 8; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADJ98065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Candida magnoliae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4-substituted 3-hydroxybutyric acid derivative; KRED; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ketoreductase; cofactor; cofactor regeneration system; nucleophile; 4-nucleophile substituted-3-hydroxybutyric acid amide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4-halo-3-ketobutyric acid ester; halohydrin dehalogenase; cya4-nucleophile substituted 3-hydroxybutyric acid ester; amide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-AUG-2003; 2003WO-US025263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4-cyano-3-hydroxybutyric acid ester;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ketoreductase 4 (KRED CR2-4) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CODE-) CODEXIS INC
                                                                                                                                                                                       Local
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      83
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                                                                                                                                                                    99;
                                                                                                                                                                                       Similarity
---KVKAYKANVSSSDAVKQTIEQQIKDFGHLDIVVAN-AGIPWTKGAYIDQDDDKHFDQ
                                      EVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAG--YCENFPCEDYPAKNAEK 125
                                                                                 FKLNGKVASITGSSSGIGYALAEAFAQVGADVAIWYNSHDATGKAEALAKKYGV-----
                                                                                                                         FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK 67
                                                                                                                                                                                                                                                   283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grate JH,
                                                                                                                                                                    Conservative
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2003US-00402436.
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70
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                                                                                                                                                                  48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprises contacting 4-halo-3-hydroxybutyric
                                                                                                                                                                                     Score 378; DB 8;
Pred. No. 3.9e-30;
                                                                                                                                                                  Mismatches 100;
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halohydrin dehalogenase; cyanide;
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                                                                                                                                                                                                      Length 283;
                                                                                                                                                                  Indels
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MVKVNLLGSLYVS----QAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAG 181

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ARBSULT 12
ADJ988
AC ADJ98
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KW 4
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The present invention describes a method (M1) for producing 4-cyano-3-CC hydroxybutyric acid ester (I) from a 4-halo-3-hydroxybutyric acid ester (II) or 4-halo-3-ketobutyric acid ester (III), comprising providing (II) CC or (III), and contacting (II) with a halohydrin dehalogenase and cyanide under conditions sufficient to form a reaction mixture for converting (II) to (I). Also described: (1) producing (N2) a 4-nucleophile CC substituted 3-hydroxybutyric acid ester or amide from (II) or amide, CC or amide with a halohydrin dehalogenase and a nucleophile under CC conditions suitable to form a reaction mixture for converting (II) or amide to a 4-nucleophile substituted-3-hydroxybutyric acid or amide; or (C) contacting (III) or amide with a ketoreductase, a cofactor, a CC cofactor regeneration system, a nucleophile and a halohydrin dehalogenase to form a reaction mixture for converting (III) or amide; or (C) contacting (III) or system, a nucleophile and a halohydrin dehalogenase to form a reaction mixture for converting (III) or amide; and (2) a CC composition (IV) comprising halohydrin dehalogenase, a nucleophile, and (C) is useful for producing a 4-cyano-3-hydroxybutyric acid ester or amide; and (C) a cid ester from a 4-halo-3-hydroxybutyric acid ester or 4-halo-3-cC ketobutyric acid ester. (M2) is useful for producing a 4-nucleophile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ketoreductase; cofactor; cofactor regeneration system; nucleophile; 4-nucleophile substituted-3-hydroxybutyric acid amide; 4-substituted 3-hydroxybutyric acid derivative; KRED; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 2; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing 4-cyano-3-hydroxybutyric acid ester from 4-halo-3-hydroxybutyric acid ester, comprises contacting 4-halo-3-hydroxybutyric acid ester with halohydrin dehalogenase and cyanide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2002;
11-AUG-2003;
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4-nucleophile substituted 3-hydroxybutyric acid ester; amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4-cyano-3-hydroxybutyric acid ester;
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)B; ADJ98059.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gruber JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4-halo-3-hydroxybutyric acid
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                                                                                                                                                                                                                               Davis SC,
Newman LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4-halo-3-ketobutyric acid ester; halohydrin dehalogenase; cyanide; 4-nucleophile substituted 3-hydroxybutyric acid ester; amide; ketoreductase; cofactor; cofactor regeneration system; nucleophile; 4-nucleophile substituted 3-hydroxybutyric acid amide; 4-substituted 3-hydroxybutyric acid derivative; KRED; enzyme.
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11-AUG-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVGAYLFLASD-AGSYATGTDIIVDGGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YIGAVLYLLSESAASYTTGASLLVDGGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRHFAKSLAVEFAPF-ARVNSVSPGYINTEISDFV---PQETQNKWWSLVPLGRGGETAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVDVDLKGVGYVAKHAGRHFRERFEKEGKKGA-LVFTASMSGHIVNVPQFQATYNAAKAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK
                                                                                                                                                                                                                               Grate JH,
Sheldon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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2003US-00402436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.7%;
36.8%;
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                                                                                                                                                                                                                               Gray DR
                                                                                                                                                                                                                       √ DR,
~ LA;
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Pred. No. 3.9e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                            Gruber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4-halo-3-hydroxybutyric acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270
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                                                                                                                                                                                                                                                               Huisman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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h is used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ester;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
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Producing 4-cyano-3-hydroxybutyric acid ester from 4-halo-3-hydroxybutyric acid ester, comprises contacting 4-halo-3-hyd acid ester with halohydrin dehalogenase and cyanide.

4-halo-3-hydroxybutyric

Example 1; SEQ ID NO 6; 168pp; English

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Best Local S
Matches 99
                                                                                                               Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; pathogen tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to form a reaction mixture for converting (III) or amide to a 4-nucleophile substituted.3-hydroxybutyric acid ester or amide; and (2) composition (IV) comprising halohydrin dehalogenase, a nucleophile, are (I) or amide. (M1) is useful for producing a 4-cyano-3-hydroxybutyric acid ester from a 4-halo-3-hydroxybutyric acid ester or 4-halo-3-ketobutyric acid ester. (M2) is useful for producing a 4-nucleophile substituted-3-hydroxybutyric acid ester or amide. (M1) and (M2) are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             under conditions sufficient to form a reaction mixture for converting (II) to (I). Also described: (I) producing (M2) a 4-nucleophile substituted 3-hydroxybutyric acid ester or amide from (II) or amide, comprising: (a) providing (II), (III) or amide; and (b) contacting (II) or amide with a halohydrin dehalogenase and a nucleophile under conditions suitable to form a reaction mixture for converting (II) or amide to a 4-nucleophile substituted-3-hydroxybutyric acid or amide; or (c) contacting (III) or amide with a ketoreductase, a cofactor, a cofactor regeneration system, a nucleophile and a halohydrin dehalogenase to form a reaction mixture for converting (III) or amide with a ketoreductase.
US2003233675-A1
                                                                                                                                                                                                                                                                                              Bacterial polypeptide #11548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADS22515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for producing 4-substituted 3-hydroxybutyric acid derivatives. The present sequence represents a ketoreductase (KRED), which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method (M1) for producing 4-cyano-3-hydroxybutyric acid ester (I) from a 4-halo-3-hydroxybutyric acid ester (II) or 4-halo-3-ketobutyric acid ester (III), comprising providing (II) or (III), and contacting (II) with a halohydrin dehalogenase and cyanide
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                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; protein; 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVGAYLFLASD-AGSYATGTDIIVDGGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YIGAVLYLLSESAASYTTGASLLVDGGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRHPAKSLAVEFAPF-ARVNSVSPGYINTEISDFV---PQETQNKWWSLVPLGRGGETAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVDVDLKGVGYVAKHAGRHFRERFEKEGKKGA-LVFTASMSGHIVNVPQFQATYNAAKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MVKVNLLGSLYVS----QAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---KVKAYKANVSSSDAVKQTIEQQIKDFGHLDIVVAN-AGIPWTKGAYIDQDDDKHFDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAG--YCENFPCEDYPAKNAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKLNGKVASITGSSSGIGYALAEAFAQVGADVAIWYNSHDATGKAEALAKKYGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRFDGHLTIVTGACGGLABALIKGLLAYGSDIALLDIDQBKTAAKQABYHKYATBELKLK
                                                                                             polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.7%; Score 378; DB 8; 36.8%; Pred. No. 3.9e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                : property;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
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PAIFLLSD-AASFVTGVDLLVDGGFCCW AVLYLLSESAASYTTGASLLVDGGFTSW

253 272 172 188 114

> TLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNR---WISGIPQQRMSEPKEYIG DINLKGVFLSCQAEANAMLKNG-RGA-IVNIASMSGVIVNRGLMQCHYNASKAGVIHMSK

187 171

127 57

113

SMAMEWVGRGIRVNTISPGYTATPM-----NTRPEMVHQTKLFEEQTPMQRMAGVDEMVG

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of
                                                                                                                                                                                                                                                                                                             of the cell cycle pathway with plant growth regulators, increased rate homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stre condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in th scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             promoter functional in a plant cell, where the promoter is position provide for expression of a polynucleotide encoding a polyneptide microbial source. The invention also relates to a transformed plan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 11548; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microbial source, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter functional in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant DNA construct comprising for expression of a polynucleotide encodi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHEN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAOY/)
                                                                                                                                                                                                                   Local
    128
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SLATER S C.
CHEN X.
GOLDMAN B S.
                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinkle GJ,
                                                                           EVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAGYCENFPCEDYPAKNAEKMV
                                                                                                                                                                                                                                                                              253
KVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAGVIHLAK
                                                                                                                   FDLSGQVALVTGAGSGIGQRIAMGLAQSGANVALLDRRTDDGLAQTADFIARAGR-----
                                                                                                                                                        FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK 67
                                        KSIQIAADVTSKQALTDAVARTQAELGALSI-AVNAAGIANANPAEEMEESQFQTMM
                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  relates to a recombinant DNA tional in a plant cell, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Slater
                                                                                                                                                                                                                 26.6%; Score 376; DB 8; 35.8%; Pred. No. 5.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 truct comprising a promoter positioned to provi
nucleotide encoding a polypeptide from a
for producing plants with improved properties.
                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sc,
                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen
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                                                                                                                                                                                                                                 Length 253;
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                                                                                                                                                                                                                                                                                                                                                                                                                  one stress
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ANDUSH ADJ98104
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                                                          Cunder conditions sufficient to form a reaction mixture for converting (II) to (I). Also described: (I) producing (M2) a 4-nucleophile (C comprising: (a) providing (II) producing (M2) a 4-nucleophile (C comprising: (a) providing (II) or amide; and (b) contacting (II) or amide with a halohydrin dehalogenase and a nucleophile under (C conditions suitable to form a reaction mixture for converting (II) or amide to a 4-nucleophile substituted-3-hydroxybutyric acid or amide; or (c) contacting (III) or amide with a ketoreductase, a cofactor, a (c) contacting (III) or amide with a ketoreductase, a cofactor, a (c) contacting (III) or amide with a ketoreductase, a cofactor, a (c) contacting (III) or amide with a ketoreductase, a nucleophile and (2) a (c) form a reaction mixture for converting (III) or amide; and (2) a (c) form a reaction mixture for converting (III) or amide; and (2) a (c) form a feation mixture for converting (III) or amide; and (2) a (c) form a reaction mixture for converting (III) or amide; and (2) a (c) form a reaction for producing a 4-cyano-3-hydroxybutyric acid ester or 4-halo-3-hydroxybutyric acid ester or 4-halo-3-c) (c) form a 4-halo-3-hydroxybutyric acid ester or 4-hydroxybutyric acid ester or 4-hydroxybutyric acid ester or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method (M1) for producing 4-cyano-3-hydroxybutyric acid ester (I) from a 4-halo-3-hydroxybutyric acid ester (II), cor4-halo-3-ketobutyric acid ester (III), comprising providing (II) or (III), and contacting (II) with a halohydrin dehalogenase and cyanide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 46; 168pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid ester with halohydrin dehalogenase and cyanide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Producing 4-cyano-3-hydroxybutyric acid ester from 4-halo-3-hydroxybutyric acid ester, comprises contacting 4-halo-3-hyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Newman LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Davis SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2002;
11-AUG-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-AUG-2003; 2003WO-US025263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4-substituted 3-hydroxybutyric acid derivative; KRED; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4-cyano-3-hydroxybutyric acid ester; 4-halo-3-hydroxybutyric acid ester; 4-halo-3-ketobutyric acid ester; halohydrin dehalogenase; cyanide; 4-nalo-3-ketobutyric acid ester; halohydrin dehalogenase; cyanide; 4-nucleophile substituted 3-hydroxybutyric acid ester; amide; ketoreductase; cofactor; cofactor regeneration system; nucleophile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ketoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ98104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ98104 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CODE-) CODEXIS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -nucleophile substituted-3-hydroxybutyric acid amide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2004-238752/22
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Sheldon
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2003US-00402436.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprises contacting 4-halo-3-hydroxybutyric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gruber JM,
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Best Loca Matches

Local Similarity nes 99; Conserv

Conservative

26.6%; Score 376; DB 8; Length 283; 36.8%; Pred. No. 6.3e-30; Live 48; Mismatches 100; Indels

22;

Gaps

8

Query Match

Sequence 283

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198
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254
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                                                                                              VIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPKE
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LVGAYLFLASD-AGSYATGTDIIVDGGYT
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                                 270
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Search completed: July Job time : 163 secs 9, 2005, 10:27:53 δ 밁 ঠ 뭐 S

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
                                                                                                                                                        Database
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1415
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Issued_Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | | | ; | accept Parket |
|-------|--|---|---|---|--|
| 989 | 8 : | 231 | N i | -08-336- | Sequence 7, Appli |
| 686 | 8 | 231 | 4 | -09-184-965-7 | Sequence 7, Appli |
| 586 | | 282 | 4 | -09-248- | e 14: |
| 378 | | 283 | w | -012-1 | e 1, |
| 378 | • | 283 | 4 | -09-777-157A- | Ø |
| 378 | | 283 | 4 | -09-734-237B- | e 70 |
| 372.5 | • | 308 | 4 | -09-248-796A-1659 | e 16 |
| 344 | | 316 | 4 | -489-039A-1299 | e 12990, |
| 340.5 | • | 257 | w | -001C- | e 3562, |
| | | 256 | 4 | -991A- | Sequence 30474, A |
| • | • | 262 | w | -09-363-189B- | e 6, |
| 312.5 | • | 292 | w | -09-468-738A- | N |
| • | 22.1 | 292 | 4 | US-09-940-019-2 | Ф 22 , |
| ٠ | • | 292 | 4. | US-09-940-037A-2 | e 2 |
| • | | 296 | w | US-09-468-738A-23 | Sequence 23, Appl |
| • | | 296 | 4 | US-09-940-019-23 | e 23, |
| 312.5 | | 296 | 4 | US-09-940-037A-23 | e 23, |
| 307 | • | 251 | 4. | US-09-922-501-16 | æ |
| 302 | | 275 | 4 | -532A- | e 4809 |
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| 290 | • | 258 | w | 04-358- | æ |
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| 290 | • | 258 | 4 | -230-562- | e 12 |
| 289 | • | 256 | μ | -594-808E | e 7, |
| 282 | • | 290 | 4. | -09-248- | Sequence 16592, A |
| 279 | • | 303 | w | -09-002- | e 1, |
| 279 | 19.7 | 303 | 4 | US-09-481-277-1 | Ļ |
| | 686 686 378 378 378 372.5 321.5 312. | 86 48.5 86 48.5 86 41.4 86 41.4 86 41.4 86 26.7 78 26.7 78 26.7 79 22.1 10 | 231 86 48.5 231 86 41.4 282 86 41.4 282 87 26.7 283 78 26.7 283 78 26.7 283 78 26.7 283 78 26.7 283 79 22.1 257 5 22.1 252 5 22.1 252 5 22.1 252 5 22.1 252 6 20.1 252 7 20.5 22.1 252 7 20.5 22.1 252 8 20.5 22.1 252 8 20.5 258 9 0 20.5 258 | 231 86 48.5 231 86 41.4 282 86 41.4 282 87 26.7 283 78 26.7 283 78 26.7 283 78 26.7 283 78 26.7 283 79 22.1 257 5 22.1 252 5 22.1 252 5 22.1 252 5 22.1 252 6 20.1 252 7 20.5 22.1 252 7 20.5 22.1 252 8 20.5 22.1 252 8 20.5 258 9 0 20.5 258 | 86 48.5 231 2 US-08-336-198C-7 86 48.5 231 4 US-09-184-965-7 86 41.4 282 4 US-09-248-796A-1413 78 26.7 283 3 US-09-367-012-1 78 26.7 283 3 US-09-377-157A-1 78 26.7 283 4 US-09-777-157A-1 78 26.7 283 4 US-09-78-1659 79 24.1 257 3 US-09-48-796A-1659 79 25.2 26.3 308 4 US-09-252-991A-2047 79 26.3 308 4 US-09-252-991A-2047 79 19.7 303 4 US-09-262-291A-2047 79 19.7 303 4 US-09-262-291A-2047 79 19.7 303 4 US-09-262-396A-1659 79 19.7 303 4 US-09-481-277-1 |

| 279 19.7 32.2 4 US-09-816-760-11 279 19.7 32.2 4 US-09-818-561-11 273.5 19.3 29.0 4 US-09-818-561-11 270.5 19.1 269 4 US-09-134-000C-4929 268 18.9 262 4 US-09-328-352-5742 265.5 18.8 253 4 US-09-70-767-41628 264.5 18.7 274 3 US-09-134-001C-4431 264.5 18.7 274 3 US-09-134-001C-4431 265.1 18.6 261 4 US-09-779-7791 262 18.5 30.3 4 US-09-818-352-7791 263 18.6 261 4 US-09-818-352-352 264 18.5 30.3 4 US-09-818-353-3795 265 18.4 266 4 US-09-918-33-3795 260 18.5 30.3 4 US-09-918-58-25 261 18.4 266 4 US-09-978-758-2 261 18.4 266 4 US-09-978-758-2 269.5 18.3 259 4 US-09-978-758-2 259.5 18.3 259 4 US-09-978-758-2 308 4 US-09-978-758-2 | 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 6 |
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| 10000000000000000000000000000000000000 | 257.5 | 259.5 | 260.5 | 261 | 262 | 262 | 262 | 263 | 264.5 | 264.5 | 265.5 | 265.5 | 268 | 270.5 | 273.5 | 279 | 279 | |
| ************************************** | 18.2 | 18.3 | 18.4 | 18.4 | 18.5 | 18.5 | 18.5 | 18.6 | 18.7 | 18.7 | 18.8 | 18.8 | 18.9 | 19.1 | 19.3 | 19.7 | 19.7 | |
| 4 US-09-818-760-11 4 US-09-838-561-11 4 US-09-248-796A-16757 4 US-09-134-000C-4929 4 US-09-328-352-5742 4 US-09-548-681A-6693 4 US-09-548-01C-4431 4 US-09-134-001C-4431 5 US-09-134-001C-4431 6 US-09-134-01C-4431 7 US-09-134-01C-4431 8 US-09-134-01C-4431 9 US-09-134-01C-4431 9 US-09-10-279-382 1 US-09-10-279-382 1 US-09-818-760-13 1 US-09-818-760-13 1 US-09-978-758-2 1 US-09-978-758-2 1 US-09-489-039A-11936 | 308 | 259 | 254 | 266 | 303 | 303 | 303 | 261 | 306 | 274 | 276 | 253 | 262 | 269 | 290 | 322 | 322 | |
| US-09-818-561-11 US-09-838-561-11 US-09-838-561-11 US-09-248-796A-16757 US-09-134-000C-4929 US-09-328-352-5742 US-09-328-352-5742 US-09-134-001C-4431 US-09-114-001C-4431 US-09-110-279-382 US-09-116-760-13 US-09-388-561-13 US-09-818-561-13 US-09-818-561-13 US-09-978-758-2 US-09-978-758-2 US-09-978-758-2 US-09-978-758-2 US-09-978-758-2 | 4 | 4. | 4. | 4. | 4. | 4. | 4 | 4 | 4 | w | 4 | 4 | μ. | 4 | 4 | 4. | 4 | 4 |
| | US-09-489-039A-7802 | US-09-489-039A-11936 | US-09-978-758-2 | US-09-107-433-3795 | US-09-838-561-13 | US-09-816-760-13 | US-09-634-955B-25 | US-09-328-352-7731 | US-09-710-279-382 | US-09-134-001C-4431 | US-09-270-767-41628 | US-09-543-681A-6693 | US-09-328-352-5742 | US-09-134-000C-4929 | US-09-248-796A-16757 | US-09-838-561-11 | US-09-816-760-11 | (で) ない 一つしま 一人 ししじ 一 本本 |
| | 7802, Ap | 11936, 1 | Appli | 3795, Ap | | 13, App1 | 25, App] | 7731, Ag | 382, App | 4431, A | 41628, 1 | 6693, AI | 5742, A | 4929, A | 75 | 11, App] | • | יייי אלעלי |

ALIGNMENTS

RESULT 1

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US-08-336-198C-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-336-198C-7
Query Match 48.5%; Score 686; DB 2; I Best Local Similarity 55.6%; Pred. No. 2.2e-67; Matches 130; Conservative 49; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application Patent No. 5866382
GENERAL INFORMATION:
                                                                                                                                                                                   TELEFAX: 703-205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acid
                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEPAX: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION US/08/336,198C
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
CCARSIFICATION: 435
                                                                                                                LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 N. Washington St.
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hahn-Hagerdal Barbei
APPLICANT: Waldfridsson, Mats
APPLICANT: Airaksinen, Ulla
TITLE OF INVENTION: XYLOSE UTILIZATION BY RECOMBINANT YEASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22046-3487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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Penttila, Merja
Ojamo, Heikki
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                                               Length 231;
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US-09-184-965-7
                                                                                                                                               US-09-184-965-7
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Patent No. 6582944
                                                                                                                 Query Match
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                                                                                                                                                                                                                                  TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
                                                                                                                                                                                                                                                             NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEPAX: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart,
STREET: 301 N. Washington &
CITY: Falls Church
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APPLICANT: Airaksir
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                    FILING DATE: 03-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                   Local Similarity
                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MILERTKSAAK--EVLGWGEETLKGEHASAIGQVSAWSCNIGDAEAVDATFSSINEHHGK
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LPLHLVNTAGYCENFPCEDYPAKNAEKMVKVNLLGSLYVSQAFAKPLIKEGIKGASVVLI 158
                            MNLERTKSAAK--EVLGWGEETLKGEHASAIGQVSAWSCNIGDAEAVDATFSSINEHHGK 58
                                                         LDIDQEKTAAKQAEYHKYATEELKLKEVPKMG---SYACDISDSDTVHKVFAQVAKDFGK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virginia
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VENTION: XYLOSE UTILIZATION BY RECOMBINANT YEASTS
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Waldfridsson, Mats
Airaksinen, Ulla
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Ojamo, Heikki
                                                                                       Conservative
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                                                                                                                                                            protein
                                                                                                  48.5%; Score 686; DB 4; Length 231; 55.6%; Pred. No. 2.2e-67;
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                                                                                       Gaps
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELITITE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14132
LENGTH: 282
                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Yasohara, Yoshihiko
APPLICANT: Kazaki, No. 6218156iyuki
APPLICANT: Hasegawa, Junzo
APPLICANT: Wada, Masaru
APPLICANT: Shimizu, Sakayu
APPLICANT: Kataoka, Michihiko
APPLICANT: Yamamoto, Kazuhiko
APPLICANT: Yamamoto, Kazuhiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14132
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US-09-248-796A-14132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 113;
                                                                                                                                                                                                                                                                                                                                       sequence 1, Application US/09367012
Patent No. 6218156
               APPLICANT: Kawabata, Hiroshi
APPLICANT: Kita, Keiko
TITLE OF INVENTION: No. 6218156el carbonyl reductase,
TITLE OF INVENTION: for using such reductase and gene
FILE REFERENCE: S72030PCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 NAEKMVKVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 IPTFRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGKYESPIGQVSAWSCNIGDAEAVDLTFKAINEHHGKISSVLVNTAGYAENFPAEEYPAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIHLAKTLACEWAKYNIRVNSLNPGYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIHLARSLACEWAKYNIRVNTLSPGHI 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAENLMKVNGLGSFYVSQAFARPLIQNNMTG-SIILIGSMSGTIVNDPQPQCMYNMSKAG
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NUMBER: US/09/367,012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.4%; Score 586; DB 4; Length 282; 54.6%; Pred. No. 3.5e-56; Dred. No. 3.5e-56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
                                                                        gene coding same,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RELATING TO CANDIDA ALBICANS
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                                                                             and method
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FILE REFERENCE: 068383.0110
CURRENT APPLICATION NUMBER: US/09/777,157A
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/367,012
PRIOR FILING DATE: 1999-11-24
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 8
SOPTWARE: Patentin version 3.0
SEQ ID NO 1
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                                                                                                                                                                       ; LENGTH: 283
; TYPE: PRT
; ORGANISM: Candida magnoliae
US-09-777-157A-1
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                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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EARLIER APPLICATION NUMBER: PCT/JP97/03051
EARLIER FILING DATE: 1997-09-01
NUMBER OF SEQ ID NOS: 8
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kawabata
APPLICANT: Kita, Ke
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yasohara, APPLICANT: Kizaki, N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 283
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No. 6448052
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EVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAG--YCENFPCEDYPAKNAEK 125
                                 FKLNGKVASITGSSSGIGYALAEAFAQVGADVAIWYNSHDATGKAEALAKKYGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVGAYLFLASD-AGSYATGTDIIVDGGYT
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                                                                 FREDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09777157A
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Katoka, Michihiko
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Kawabata, Hiroshi
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                                                                                                       Conservative
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                                                                                                26.7%; Score 378; DB 4; Length 283; 36.8%; Pred. No. 3.7e-33; tive 48; Mismatches 100; Indels
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                 Sequence 16593, Application US/09248796A
Patent No. 6747137
GENERRAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 26.7%;
Best Local Similarity 36.8%;
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GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/248,796A
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PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 79
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CURRENT APPLICATION NUMBER: US/09/734,237B
CURRENT FILING DATE: 2000-12-08
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APPLICANT: Hua, Ling
TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED
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ORGANISM: Candida magnoliae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 MYKVNLLGSLYVS----QAFAKPLIKEGIKGASVYLIGSMSGAIVNDPQNQVVYNMSKAG 181
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                                                                                                                                                                                                                                                                                                                             VRHFAKSLAVEFAPF-ARVNSVSPGYINTEISDFV---PQETQNKWWSLVPLGRGGETAE
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Pred. No. 3.7e-33;
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CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 16593
LENGTH: 308
TYPE: PRT
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US-09-489-039A-12990
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LENGTH: 316
TYPE: PRT
                                                                                                                                                                                                        Query Match
Best Local S
Matches 87
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Best Local
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                               09-489-039A-12990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                               ORGANISM: Klebsiella pneumoniae
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 173
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| 87; Conserv
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                   EKMYKVNILGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAGVI 183
                                                                                                                                                                      FRFDGHLT1VTGACGGLAEAL1KGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK
 QRVIDINLTGVWNSCKAEAELMLESG--GGSIINIASMSGIIVNRGLDQAHYNCSKAGVI
                                                                    -IESIGGQACSYNGDVRQIADLRAAVALAKSRYGRLDI-AVNAAGIANANPALEMESEQW
                                                                                                     EVPKMGSYAC----DISDSDTVHKVFAQVAKDFGKLPLHLVNTAGYCENFPCEDYPAKNA 123
                                                                                                                                       FSLRDRVAFVTGAGSGIGQTIACSLASAGARVVCFDLRDDGGLAETVSH------
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR RILING DATE: 1997-11-08
PRIOR RILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
NUMBER OF SEQ ID NOS: 5674
LENGTH: 257
LENGTH: 257
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        APPLICANT: MARC J. RUBERFIELD Et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEO ID NO 30.70.70
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Best Local
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SEQ ID NO 30474
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es 82; Conserv
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; Pred. No. 4.4e-29;
64; Mismatches 105;
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US-09-363-189B-6
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APPLICANT:
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TITLE OF INVENTION: XYLITOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
FILE REFERENCE: 0010-1024-0
CURRENT APPLICATION NUMBER: US/09/363,189B
CURRENT FILING DATE: 1999-07-26
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ORGANISM: Pseudomonas
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TYPE: PRT
                                                                                                                                                                                                                                                                                                  / Match 22.7%; Score 321.5; DB 3; Length 262;
Local Similarity 31.0%; Pred. No. 5.8e-27;
1es 86; Conservative 53; Mismatches 103; Indels 35
                                         188
                                                                              114
                                                                                              128 KVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAGVIHLAK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 SMTKVFAKECAQFGIRCNALLFGLTDTKFASALVK-NDAIRNLALQRIPLKRVAEPSEMA
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                                                                        TINVTGAFHVLKAVSROMITONY--GRIVNTASMAG--VKGPPNMAAYGASKGAIIALTE 169
                                                                                                                                                                                                                                                              RFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLKE 68
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                                 TLACEWAKYNIRVNSLNPGYIYGP-----LTKNVINGNE-----ELYNRWISGI 231
                                                                                                                                                   ---ARSYVCDVTSEEAVIGTVDSVVRDFGKIDF-LFNNAGYQGAFAPVQDYPSDDFARVL 113
                                                                                                                                                                                                                           KFNGKVCLVTGAGGNIGLATALRLAEEGTAIALLDMNREALEKAEASVREKGVB-----
                                                                                                                                                                                      VPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAGYCENF-PCEDYPAKNAEKMV 127
TAALDLAPYNIRVNAISPGYM-GPGFMWERQVELQAKV--GSQYFSTDPKVVAQQMIGSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TONOUCHI, NAOTO SUZUKI, SHUNICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUGIYAMA, MASAKAZU
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34.7%;
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APPLICANT: Kimoto, No. 6416986ihiro
APPLICANT: Yamamoto, Hiroaki
APPLICANT: Yamamoto, Hiroaki
APPLICANT: Mitsuhashi, Kazuya
TITLE OF INVENTION: NOVEL CARBONYL REDUCTASI
TITLE OF INVENTION: ENCODING SAID ENZYME, F
TITLE REFERENCE: 06501-050001
CURRENT APPLICATION NUMBER: US/09/940,019
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/468,738
PRIOR APPLICATION NUMBER: JP 1998-363130
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CURRENT APPLICATION NUMBER: US/09/468,738A

CURRENT FILING DATE: 1999-12-21

PRIOR APPLICATION NUMBER: JP 1999-171160

PRIOR FILING DATE: 1999-06-17

PRIOR APPLICATION NUMBER: JP 1998-363130

PRIOR FILING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin Ver: 2.0, reformatted usin
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GENERAL INFORMATION:
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APPLICANT: Yamamoto, Hiroaki
APPLICANT: Mitsuhashi, Kazuya
TITLE OF INVENTION: NOVEL CARBONYL
TITLE OF INVENTION: ENCODING SAID
TITLE OF INVENTION: ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 292
TYPE: PRT
ORGANISM: Kluyveromyces aestuarii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 --- ENFPCEDYPAKNAEKMVKVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVN 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYNRWISGIPQQRMSEPKEYIGAVLYLLSESAASYTTGASLLVDGGFT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPNYQTCYNASKAAVRHMAKGFAVEFAHLTNPAGKIRCNSVSPGYTDTALSAFV---PVB
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                                                                                                                                                                                                                                                                                                                               Application US/09940019
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Pred. No. 6.9e-26;
Pred. No. 6.9e-26;
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ENZYME, AN
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                                                                                                                                                                SE, METHOD FOR PRODUCING SAID ENZYME, DI AND METHOD FOR PRODUCING ALCOHOL USING
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US-09-940-037A-2
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NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIn Ver. 2.0, reformatted using WordPerfect 5.1

SEQ ID NO 2

LENGTH: 292

TYPE: PRT

ORGANISM: Kluyveromyces aestuarii

S-09-940-019-2
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SEQ ID NO 2
LENGTH: 292
TYPE: PRT
ORGANISM: Kluyveromyces aestuarii
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Best Local Similarity 32.3%; Pred. No. 6.90
Matches 93; Conservative 50; Mismatches
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                                                                                                                                                                                            Matches
                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kimoto, No. 6485948ihiro
APPLICANT: Yamamoto, Hiroaki
APPLICANT: Mitsuhashi, Kazuya
TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING SAID ENZYME, DNA
TITLE OF INVENTION: ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL USING SA
TITLE OF INVENTION: ENZYME
                                                                                                                                                                                                                                                                     -09-940-037A-2
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 1998-363130 PRIOR FILING DATE: 1998-12-21 NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 06501-050001
CURRENT APPLICATION NUMBER: US/09/940,037A
CURRENT FILING DATE: 2000-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/468,738 PRIOR FILING DATE: 1999-12-21
                                                                                                                                                                                                              Local
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                                                                                                                                                                                                              Similarity
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                                                                                                              VPNYQTCYNASKAAVRHMAKGFAVEFAHLTNPAGKIRCNSVSPGYTDTALSAFV---PVE
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                                     LSSVLESRYGVRSKSYQVDITSSEDVKLVVAKILEDF---PDRDINTFVANAGIAWTNGS
                                                                           ---ELKLKEVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNT----AGYC----
-ENFPCEDYPAKNAEKMVKVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVN
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                            22.1%; Score 312.5; 32.3%; Pred. No. 6.9
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Search completed: July Job time : 45 secs

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APPLICANT: Kimoto, No. 6312933ihiro
APPLICANT: Yamamoto, Hiroaki
APPLICANT: Mitsuhashi, Kazuya
APPLICANT: Mitsuhashi, Kazuya
TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE,
TITLE OF INVENTION: ENCODING SAID ENZYME, ANI
TITLE OF INVENTION: ENCODING SAID ENZYME, ANI
TITLE OF INVENTION: ENCODING SAID ENZYME, ANI
TITLE OF INVENTION: ENZYME
FILE REFERENCE: 06501-050001
CURRENT APPLICATION NUMBER: US/09/468,738A
CURRENT FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: JP 1999-171160
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: JP 1998-363130
PRIOR FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0, reformatted usin
SEQ ID NO 23
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US-09-468-738A-23
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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TYPE: PRT
ORGANISM: Kluyveromyces aestuarii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 ILNENATPDVW-----KRVMDVNVQGTYHCAKYVAEVFKQQG--HGNLILTASMSSYISN
                                                                                  191
                                                                                                                           168
  248
                                                                                                                                                                138 ILNENATPDVW-----KRVMDVNVQGTYHCAKYVAEVFKQQG--HGNLILTASMSSYISN 190
                                                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                          63 ---ELKLKEVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNT----AGYC----
                                                                                                                                                                                                                                                                                                                                                                        3 DYIPTFREDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATE 62
                                                                                                                                                                                                        ---ENFPCEDYPAKNAEKMVKVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVN 167
                                                                                                                                                                                                                                                 LSSVLBSRYGVRSKSYQVDITSSEDVKLVVAKILEDF---PDRDINTFVANAGIAWTNGS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYNRWISGIPQQRMSEPKEYIGAVLYLLSESAASYTTGASLLVDGGFT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPQNQVVYNMSKAGVIHLAKTLACEWAKY-----NIRVNSLNPGYIYGPLTKNVINGNEE
                                  LYNRWISGIPQQRMSEPKEYIGAVLYLLSESAASYTTGASLLVDGGFT 270
                                                                                                                                                                                                                                                                                                                                      NYLSLFSQKGKLTVITGGAGAIGGALCEGFASCGSDVVILD------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPNYQTCYNASKAAVRHMAKGFAVEFAHLTNPAGKIRCNSVSPGYTDTALSAFV---PVE
QRAQWWGLTPMGREALPQELVGAYLYLASD-AASFTNGCDIQVDGGYT
                                                                                                                 DPQNQVVYNMSKAGVIHLAKTLACEWAKY-----NIRVNSLNPGYIYGPLTKNVINGNEE 222
                                                                                  VPNYQTCYNASKAAVRHMAKGFAVEFAHLTNPAGKIRCNSVSPGYTDTALSAFV---PVE
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 312.5; DB 
Pred. No. 7e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                          98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 296;
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and is derived
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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               US-10-720-018-2
US-10-369-493-2923
US-10-369-493-13036
US-10-639-159-42
US-10-639-159-60
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            Sequence 2, Appli
Sequence 2923, Ap
Sequence 13036, A
Sequence 40, Appl
Sequence 118, App
                                                                                                                                                                                                                                              Description
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| 45 | 44 | 43 | 42 | 41 | 40 | 9 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 |
|----------------|-----------------|-----------------|----------------|-----------------|--------------|---------------|------------|----------|------------|-------------------|----------|-------------|--------------|---------------|---------------|---------------|----------------|--------------|----------------|--------------|---------------|--------------|---------------|--------------|--------------|--------------|----------------|-----------------|----------------|-----------------|-----------------|----------------|-------------------|
| 358.5 | σ | σ | 367 | σ | σ | ~ | J | 373 | 373 | 373 | 373 | 373 | 373 | 373 | 374 | 374 | 7 | J | ٠, | 7 | 7 | J | J | J | ~ | J | J | J | J | J | 378 | J | J |
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| 266 | 251 | 263 | 283 | 283 | 251 | 283 | 283 | 283 | 283 | 283 | 283 | 283 | 283 | 283 | 283 | 283 | 245 | 283 | 283 | 283 | 283 | 283 | 283 | 283 | 283 | 253 | 283 | 283 | 283 | 283 | 283 | 283 | 283 |
| 18 | 15 | 14 | 16 | 16 | 15 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 15 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 16 | 15 | 16 | 16 | 16 | 16 | 16 | 16 | 10 |
| S-10-508-681-3 | -10-369-493-142 | -10-128-714-82 | -10-782-258-4 | -10-639-159-4 | -10-369-493- | -10-782-258-5 | 0-639-159- | 82-258-1 | 0-782-258- | -10-7 | 82-258-5 | 0-639-159-5 | -10-639-159- | -10-639-159-5 | -10-782-258-4 | -10-639-159-4 | -10-369-493-33 | -10-782-258- | -10-782-258-11 | -10-782-258- | -10-782-258-4 | -10-782-258- | -10-639-159-5 | -10-639-159- | -10-639-159- | -10-369-493- | 0-782-258- | -10-782-258- | -10-782-258- | -10-639-159- | S-10-639- | -10-639-159-2 | US-09-734-237B-70 |
| quence 3, Appl | equence 14214 | equence 8283, A | equence 48, Ap | equence 48, App | equence 14: | equence 52 | e 52 | nce 11 | e 58 | Sequence 56, Appl | 50 | 58 | 56 | 50 | 44 | 44 | 33 | 12 | 11 | 54 | 46 | 4. | 54 | 46 | | 1 | equence 8, App | equence 6, Appl | quence 2, Appl | equence 8, Appl | equence 6, Appl | equence 2, App | Sequence 70, Appl |

ALIGNMENTS

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LENGTH: 272;
TYPE: PRT;
ORGANISM: Ambrosiozyma monospora
US-10-720-018-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-720-018-2
                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 272; Conservat
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Publication No. US20040132074A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Verho, Ritva
APPLICANT: Verho, Ritva
APPLICANT: Richard, Peter
APPLICANT: Renttila, Merja
APPLICANT: Penttila, Merja
TITLE OF INVENTION: New Enzyme for an in vivo and in vitro Utilisation of
TITLE OF INVENTION: carbohydrates
FILE REFERENCE: 2530-120
CURRENT APPLICATION MIMBER: US/10/720,018
CURRENT FILING DATE: 2003-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
121 KNAEKMYKVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKA 180
                                                  61
                                                                        61 TEELKLKEVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAGYCENFPCEDYPA 120
                                                                                                                                                               1 MTDYIPTFRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYA 60
                                                                                                                                       MTDYIPTEREDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYA 60
                                                                                                                                                                                                                                   Conservative
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Sequence 1,

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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slatear, Steven C.
APPLICANT: Slatear, Steven S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2923
LENGTH: 257
TYPE: PRT
ORGANISM: Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2923, Application US/10369493
Publication No. US20030233675A1
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                                                                                                                                                        Sequence 13036, Application US/10369493 Publication No. US20030233675A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Goldman, Barry APPLICANT: Chen, Xianfeng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQEMSEPK 240
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                                                                                                                                                                                                                                                                                                                                                                                             GVIHLAKTLACEWAKYNIRVNSLNPGYIYGPL--TKNVINGNEELYNRWISGIPQORMSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVPKMGS----YACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAG----YCENFPCEDYPA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                      EKWKKVIDVNLVG-VFLSAKAEFHAMKER-KYGKIINIASMSGHIVNKPOKOTAYNASKA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIKEKGGEADFYVGDVTKEEDCFGAVKKALDRWGKLDIG-VNNAGIGDWCE---AENYPV 110
                                                                                                                                                                                                                                                                                                                                                          GVIHLTRSLAAEWAPYGIRVNSISPGYIRTPLIESPNV----KDLVPLWLDMIPLGRLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSLKRKVALVTGGGQGIGKAIAQALAAAGAAVLIMDINEE-TARRTVE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.4%; Score 402.5; DB 1 36.9%; Pred. No. 5.1e-31; tive 50; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 15;
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                        PLANTS FOR PRODUCTION
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-8
FRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 13036
LENGTH: 211
TYPE: PRT
ORGANISM: Aspergillus nidulans
FERNTHER:
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                                                                                                                      ; OTHER INFORMATION: KRED krh215 US-10-639-159-42
                                                                                                                                                                                                                    APPLICANT: Sheldon, Roger
APPLICANT: Wang, Lia
APPLICANT: Wang, Lia
TITLE OF INVENTION: ENZYMATIC PROCESSES FOR THE PRODUCTION
TITLE OF INVENTION: OF 4-SUBSTITUTED-3-HYDROXYBUTYRIC ACID DERIVATIVES
FILE REFERENCE: 0339.210US
CURRENT FILING NATE: 2003-08-11
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: US 60/402,436
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 92
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 42
LENGTH: 283
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Best Local
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                                              Matches
                                                                 Query Match
Best Local Similarity
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APPLICANT:
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LOCATION: (1)..(211)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                               ORGANISM: Artificial Sequence PEATURE:
                                                                                                                                                                                                       TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 SQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAGVIHLAKTLACEWAKYN 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 GVPEDLMGAVTFILSD-ASKYITGADLRVDGGYT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 SEPKEYIGAVLYLLSESAASYTTGASLLVDGGFT 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DVSNPDSVNNALSEVIAKHGKID-HLVTSAGFTENFDAISYPYDRMQKLWGVNVDGTYLF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 88
                                                97;
        8 FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grate, John H.
Gray, David R.
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                                                Conservative
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                                                                 26.9%;
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                                              52;
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Pred. No. 1.7e-30;
                                              Score 381; DB 16;
Pred. No. 7.9e-29;
2; Mismatches 98;
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                                                                                     Length 283;
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RESULT 5
US-10-639-159-60
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PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 60
LENGTH: 283
                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Newman, Lisa M.
APPLICANT: Sheldon, Roger
APPLICANT: Wang, Li A
APPLICANT: Wang, Li A
TITLE OF INVENTION: ENZYMATIC PROCESSES FOR THE PRODUCTION
TITLE OF INVENTION: OF 4-SUBSTITUTED-3-HYDROXYBUTYRIC ACID DERIVATIVES
FILE REFERENCE: 0339.210US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/639,159
CURRENT FILING DATE: 2003-08-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Davis, S. Christopher APPLICANT: Grate, John H. APPLICANT: Gray, David R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: KRED krh495
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242 YIGAVLYLLSESAASYTTGASLLVDGGFT 270 :|| |:| |:| || |:| ::||||:|
                                                                                                     182
                                                                                                                                            139 VIDVDLKGVGYVAKHAGRHYRERFEKEGIKGA-LIFTASVSGHIVNIPQFQATYNAAKAG
                                                                                                                                                                                  126 MVKVNILGSLYVS----QAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAG 181
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                                                                                                                                                                                                                        83 ---KVKAYKANVSSSDAVKQTIEQQIKDFGHLDIVVAN-AGIPWTKGAYIDQDDDKHFDQ 138
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                                                                                                                                                                                                                                                                                                                                                                                                          h 26.9%; Score 381; DB 16; Similarity 36.1%; Pred. No. 7.9e-29;
                                                             VRHFAKSLAVEFAPF-ARVNSVSPGYINTEISDFV---PQETQNKWWSLVPLGRGGETAE
                                                                                                   VIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPKE 241
                                                                                                                                                                                                                                                                EVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAG--YCENFPCEDYPAKNAEK 125
                                                                                                                                                                                                                                                                                                                                           FRFDGHLTIVTGACGGLABALIKGLLAYGSDIALLDIDQEKTAAKQABYHKYATEELKLK
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                                                                                                                                                                                                                                                                                                         FKLNGKVASITGSSSGIGYALAEAFAQVGADVAIWYNSQDATGKAEALAKKYGV-----
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Huisman, Gjalt W.
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No. US20040137585A1
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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              Sequence 60, Application US/1078258
Publication No. US20040214297A1
GENERAL INFORMATION:
APPLICANT: Davis, S. Christopher
APPLICANT: Grate, John H.
APPLICANT: Gray, David R.
APPLICANT: Gray, David M.
APPLICANT: Huisman, Gjalt W.
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US-10-782-258-60
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Best Local
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Steven K.

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US-10-782-258-42
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Publication No. US20040214297A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Enzymatic Processes for the Production
TITLE OF INVENTION: of 4-Substituted 3-Hydroxybutyric Acid Derivatives .
TITLE OF INVENTION: vicinal Cyano, Hydroxy-substituted Carboxylic Acid .
FILE REFERENCE: 0339.310US
CURRENT APPLICATION NUMBER: US/10/782,258
CURRENT FILING DATE: 2004-02-18
PRIOR APPLICATION NUMBER: US 10/639,159
PRIOR PILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: US 60/402,436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Davis, S. Christopher APPLICANT: Grate, John H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 283
TYPE: PRT
ORGANISM: Artificial Sequence
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OTHER INFORMATION: KRED krh215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                           242 YIGAVLYLLSESAASYTTGASLLVDGGFT 270
                                                                                                                                             182 VIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPKE 241
                                                                                                                                                                                              139 VIDVDLKGVGYVAKHAGRHYRERFEKEGIKGA-LIFTASVSGHIVNIPQFQATYNAAKAG
                                                                                                                                                                                                                                126 MVKVNLLGSLYVS----QAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAG 181
                                                                                                                                                                                                                                                                                              83 ---KVKAYKANVSSSDAVKQTIEQQIKDFGHLDIVVAN-AGIPWTKGAYIDQDDDKHFDQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97;
EVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAG--YCENFPCEDYPAKNAEK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                            FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK 67
                                                                                                                                                                                                                                                                                                                                                                                           FKLNGKVASITGSSSGIGYALAEAFAQVGADVAIWYNSQDATGKAEALAKKYGV----- 82
                                                                                               VRHFAKSLAVEFAPF-ARVNSVSPGYINTEISDFV---PQETQNKWWSLVPLGRGGETAE
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Gray, David R.
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Huisman, Gjalt W.
Ma, Steven K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.9%; Score 381; DB 16; 36.1%; Pred. No. 7.9e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 283;
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Esters
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APPLICANT: Newman, Lisa M.
APPLICANT: Sheldon, Roger
IAPPLICANT: Wang, Li A.
ITILE OF INVENTION: Enzymatic Processes for the Production
ITILE OF INVENTION: Of 4-Substituted 3-Hydroxybutyric Acid Derivatives and
ITILE OF INVENTION: Vicinal Cyano, Hydroxy-substituted Carboxylic Acid Esters
ITILE REFERENCE: 0339-310US
ITILE OF INVENTION NUMBER: US/10/782,258
CURRENT APPLICATION NUMBER: US/10/782,258
CURRENT APPLICATION NUMBER: US 10/639,159
PRIOR APPLICATION NUMBER: US 10/639,159
PRIOR APPLICATION NUMBER: US 60/402,436
PRIOR FILING DATE: 2002-08-11
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 126
SOPTWARE: FastSEQ for Windows Version 4.0
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US-10-639-159-40
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APPLICANT:
APPLICANT:
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NUMBER OF SEQ ID NOS: 92
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 283
                                                                                APPLICANT: Ma, Steven K.
APPLICANT: Newman, Lisa M.
APPLICANT: Sheldon, Roger
APPLICANT: Sheldon, Roger
APPLICANT: Wang, Li A
TITLE OF INVENTION: ENZYMATIC PROCESSES FOR THE PRODUCTION
TITLE OF INVENTION: OF 4-SUBSTITUTED-3-HYDROXYBUTYRIC ACID DERIVATIVES
TILE REFERENCE: 0339.210US
CURRENT APPLICATION NUMBER: US/10/639,159
CURRENT APPLICATION NUMBER: US/60/402,436
PRIOR APPLICATION NUMBER: US 60/402,436
PRIOR FILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Davis, S. Christopher APPLICANT: Grate, John H.
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198
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LVGAYLFLASD-AGSYATGTDIIVDGGYT 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEBLKLK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRHFAKSLAVEFAPF-ARVNSVSPGYINTEISDFV---PQETQNKWWSLVPLGRGGETAE
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Huisman, Gjalt W.
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Gray, David R.
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; OTHER INFORMATION: KRED krhl33c US-10-639-159-40
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US-10-782-258-40
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Best Local Similarity
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                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 40
                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Newman, Lisa M.
APPLICANT: Sheldon, Roger
APPLICANT: Sheldon, Roger
APPLICANT: Wang, Li A.
APPLICANT: Wang, Li A.
TITLE OF INVENTION: Enzymatic Processes for the Production
TITLE OF INVENTION: of 4-Substituted 3-Hydroxybutyric Acid Derivatives
TITLE OF INVENTION: Vicinal Cyano, Hydroxy-substituted Carboxylic Acid
FILE REFERENCE: 0339.310US
CURRENT APPLICATION NUMBER: US/10/782,258
CURRENT FILING DATE: 2004-02-18
PRIOR APPLICATION NUMBER: US 10/639,159
PRIOR APPLICATION NUMBER: US 10/639,159
PRIOR APPLICATION NUMBER: US 60/402,436
DRIOR STILING DATE: 2003-08-11
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                                                                                                                                                                                                                     LENGTH: 283
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                               OTHER INFORMATION: KRED krh133c
                                                                                                                                                                                                      FEATURE:
                                                                                                  Local
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  29
                                   8 FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK 67
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                                                                                                    Similarity
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  FKLNGKVASITGSSSGIGYALAEAFAQVGADVAIWYNSQDATGKAEALAKKYGV----
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Ma, Steven K.
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Gray, David R.
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                                                                                 Conservative
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                                                                                                  26.9%; Score 380; DB 16; 36.8%; Pred. No. 9.9e-29;
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                                                                                   Mismatches
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PRIOR FILING DATE: 2003-08-11
PRIOR PPLICATION NUMBER: US 60/402,436
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 118
SEQ ID NO 118
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 118, Application US/10782258 Publication No. US20040214297A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Enzymatic Processes for the Production
TITLE OF INVENTION: of 4-Substituted 3-Hydroxybutyric Acid Derivatives
TITLE OF INVENTION: Vicinal Cyano, Hydroxy-substituted Carboxylic Acid
FILE REFERENCE: 0339.310US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Davis, S. Christopher APPLICANT: Grate, John H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/782,258
CURRENT FILING DATE: 2004-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                       Match 26.8%; Score 379; DB 16; Local Similarity 37.2%; Pred. No. 1.2e-28;
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242 YIGAVLYLLSESAASYTTGASLLVDGGFT 270
                                                                   182 VIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPKE 241
                                                                                                            139 VVDVDLKGAGYVAKHAGRHFRERFEKEGKKGA-LVFTASMSGHIVNVPQFQATYNAVKAG
                                                                                                                                              126 MVKVNLLGSLYVS----QAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAG 181
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                                                                                                                                                                                   ---KVKAYKANVSSSDAVKQTIEQQIKDFGHLDIVVAN-AGIPWTKGAYIDQDDDKHFDQ 138
                                                                                                                                                                                                                                                                                             FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK
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                                    VRHFAKSLAVEFAPF-ARVNSVSPGYINTEISDFV---PQETQNRWWSLVPLGRGGETAE
                                                                                                                                                                                                                                                         FKLNGKVASITGSNSGIGYALAEAFAQVGADVAIWYNSHDATGKABALAKKYGV-----
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Huisman, Gjalt W.
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US-09-734-237B-70
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US-09-777-157A-1
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LENGTH: 283
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CURRENT APPLICATION NUMBER: US/09/734,237B
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/494,921
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.1
SEQ ID NO 70
                                                                                                                                                                                                                                                                                                                  Sequence 70, Application US/09734237B Publication No. US20030064432A1 GENERAL INFORMATION:
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APPLICANT: Kizaki, No.
APPLICANT: Hasegawa, Jun
APPLICANT: Wada, Masaru
APPLICANT: Shimizu, Sak
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                                                                                                                                                                                APPLICANT: Rozzell, J. David
APPLICANT: Bui, Peter
APPLICANT: Hui, Ling
TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED
FILE REFERENCE: B583:40608
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ORGANISM: Candida magnoliae
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Kawabata, Hiroshi
Kita, Keiko
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Katoka, Michihiko
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APPLICANT: Wang, Li A
APPLICANT: Wang, Li A
APPLICANT: Wang, Li A
TITLE OF INVENTION: ENZYMATIC PROCESSES FOR THE PRODUCTION
TITLE OF INVENTION: OF 4-SUBSTITUTED-3-HYDROXYBUTYRIC ACID DERIVATIVES
FILE REFERENCE: 0339.210US
CURRENT APPLICATION NUMBER: US/10/639,159
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: US 60/402,436
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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Best Local Similarity
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126 MVKVNILGSLYVS----QAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAG
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                                                                 83 ---KVKAYKANVSSSDAVKQTIEQQIKDFGHLDIVVAN-AGIPWTKGAYIDQDDDKHFDQ 138
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                                                                                                     EVPKMGSYACDISDSDTVHKVFAQVAKDFGKLFLHLVNTAG--YCENFPCEDYPAKNAEK 125
                                                                                                                                                                             FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK 67
                                                                                                                                                       FKLNGKVASITGSSSGIGYALAEAFAQVGADVAIWYNSHDATGKAEALAKKYGV-----
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Newman, Lisa M.
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Gray, David R.
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                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                      26.7%; Score 378; DB 16; 36.8%; Pred. No. 1.6e-28; ative 48; Mismatches 100;
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US-10-639-159-6
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RESULT 15
US-10-639-159-8
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Best Local S
Matches 99
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Publication No. US20040137585A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sheldon, Roger
APPLICANT: Wang, Li A
APPLICANTON: ENZYMATIC PROCESSES FOR THE PRODUCTION
TITLE OF INVENTION: OF 4-SUBSTITUTED-3-HYDROXYBUTYRIC ACID DERIVATIVES
FILE REFERENCE: 0339.210US
CURRENT ENLING DATE: 035-08-11
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: US 60/402,436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Davis, S. Christopher APPLICANT: Grate, John H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Candida magnoliae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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254 LVGAYLFLASD-AGSYATGTDIIVDGGYT 281
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                                                                                                                                                                                                                                                                                     126 MYKYNLLGSLYVS----QAFAKELIKEGIKGASVYLIGSMSGAIVNDEQNQVVYNMSKAG
                                                                                                                 242 YIGAVLYLLSESAASYTTGASLLVDGGFT 270
                                                                                                                                                                                                        182 VIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPKE
                                                                                                                                                                                                                                                                                                                                                                         68 EVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAG--YCENFPCEDYPAKNAEK 125
                                                                                                                                                                                                                                                                                                                                  83 ---KVKAYKANVSSSDAVKQTIEQQIKDFGHLDIVVAN-AGIPWTKGAYIDQDDDKHFDQ 138
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LVGAYLFLASD-AGSYATGTDIIVDGGYT 281
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Gray, David R.
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Huisman, Gjalt W.
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Pred. No. 1.6e-28;
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Sequence 8, Application US/10639159
Publication No. US20040137585A1
GENERAL INFORMATION:
APPLICANT: Davis, S. Christopher
APPLICANT: Grate, John H.
APPLICANT: Gray, David R.

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APPLICANT: Gruber, John M.
APPLICANT: Huisman, Gjalt W.
APPLICANT: Ma, Steven K.
APPLICANT: Newman, Liss M.
APPLICANT: Newman, Liss M.
APPLICANT: Sheldon, Roger
APPLICANT: Wang, Li A
APPLICANT: Wang
Search completed: July 9, 2005, 10:44:43
Job time : 163 secs
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                                                                                                                                                                    182 VIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPKE 241
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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    798.5
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1415
1 MTDYIPTFRFDGH
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1: pir1:*
2: pir2:*
3: pir3:*
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    MTDYIPTFRFDGHLTIVTGA.....SAASYTTGASLLVDGGFTSW 272
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(without alignments)
638.316 Million cell updates/sec
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    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                               AH2362
T38157
D84695
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F95295
AB0812
AS7149
C87474
G87408
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JC7338

AG2809

B97588

T39164

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JC7939
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probable oxidorédu
gluconate 5-dehydr
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carbonyl reductase
                                                                                                                                                                                                                                                                           D-arabinitol 2-deh
D-arabinitol 2-deh
                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                2-deoxy-D-gluconat
                                                                                                                                                                                                                                           short chain dehydr
                                                                                                                                                                                                                                                                                                                                                                                                    D-arabinitol 2-dehydrogenase (EC 1.1.1.-) - yeast (Pichia stipitis)
C;Species: Pichia stipitis
C;Species: Pichia stipitis
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57351; S57352
R;Hallborn, J.; Walfridsson, M.; Penttilae, M.; Keraenen, S.; Hahn-Haegerdal, B.
Yeast 11, 839-847, 1995
A;Title: A short-chain dehydrogenase gene from Pichia stipitis having D-arabinitol dehyd
A;Reference number: S57351; MUID:96090133; PMID:7483848
A;Accession: S57351
A;Molecule type: DNA
A;Residues: 1-278 <HAL>
  KESOLI
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Regult No.

| probable tropinone | | | | | | |
|--------------------|--------|---|-----|------|-------|----|
| | A84695 | N | 260 | 19.4 | 274.5 | 'n |
| short-chain alcoho | G97220 | N | 267 | 19.4 | 275 | 4 |
| 2-deoxy-D-gluconat | F85936 | N | 253 | 19.5 | 275.5 | ΰ |
| 2-deoxy-D-gluconat | C91091 | N | 253 | 19.5 | 276.5 | 2 |
| probable oxidoredu | D85885 | N | 285 | 19.6 | 277 | 1 |
| probable oxidoredu | A91041 | N | 285 | 19.6 | 277 | 0 |
| probable tropinone | B84693 | N | 268 | 19.6 | 277 | 39 |
| probable tropinone | C84695 | N | 269 | 19.6 | 278 | 8 |
| probable 3-oxoacyl | A65017 | ب | 285 | 19.7 | 279 | 37 |
| probable gluconate | G96016 | N | 268 | 19.9 | 281 | 36 |
| 3-oxoacyl-(acyl ca | H72219 | N | 246 | 19.9 | 281 | 35 |
| probable tropinone | D84694 | N | 322 | 19.9 | 281.5 | 4 |
| probable tropinone | G84694 | N | 262 | 19.9 | 281.5 | 3 |
| 2,5-dichloro-2,5-c | G82644 | N | 255 | 20.1 | 284 | 32 |
| probable dehydroge | AI0406 | N | 256 | 20.1 | 285 | 31 |
| probable tropinone | C84711 | N | 262 | 20.2 | 285.5 | ö |

ALIGNMENTS

| RESULT 2 | Qy 235 RMSEPKEYIGAVLYLLSESAASYTTGASLLVDGGFTSW 272 : : : : : : : | Qy 175 YNMSKAGVIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQ 234 | Qy 115 CEDYPAKNAEKWYKVNILGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVV 174 | Qy 58 KYATEBLKLKEVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAGYCENFP 114 | Qy 3 DYIPTFRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYH 57 | Query Match 56.4%; Score 798.5; DB 2; Length 278; Best Local Similarity 54.3%; Pred. No. 1.1e-55; Matches 151; Conservative 54; Mismatches 64; Indels 9; Gaps 3; | A;Gene: ARDH C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology C;Superfamily: ribitol dehydrogenase; C;Keywords: NAD; oxidoreductase R;17-212/Domain: short-chain alcohol dehydrogenase homology <sadh> F;17-47/Region: beta-alpha-beta NAD nucleotide-binding fold</sadh> | A;Molecule type: mRNA A;Residues: 1-278 <ham> A;Residues: 1-278 <ham> A;Cross-references: EMBL:Z46866; NID:g758241; PIDN:CAA86939.1; PID:g763164 A;Experimental source: strain CBS 6054 C;Genetics:</ham></ham> | A;Residues: 1-278 <hal> A;Cross-references: UNIPROT:P50167; EMBL:Z46866; NID:g758241; PIDN:CAA86939.1; PID:g7631 A;Accession: S57352</hal> |
|----------|---|---|---|---|---|--|---|---|--|

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D-arabinitol 2-dehydrogenase (EC 1.1.1.-) - yeast (Candida tropicalis)
N;Alternate names: D-arabinitol dehydrogenase (ribulose-forming)
C;Species: Candida tropicalis
C;Date: 13-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: JC4041; PC4017
R;Murray, J.S.; Wong, M.L.; Miyada, C.G.; Switchenko, A.C.; Goodman, T.C.; Wong,
Gene 155, 133-128, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: interconverts D-arabinitol plus NAD with D-ribulose plus C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase C;Keywords: NAD; oxidoreductase F;21-216/Domain: short-chain alcohol dehydrogenase homology <SADH> F;21-51/Region: beta-alpha-beta NAD nucleotide-binding fold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 110-129;198-205;206-209;225-234 <MU2>
C;Comment: This enzyme is a NAD-dependent short-chain-alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: JC4041
A;Molecule type: DNA
A;Residues: 1-282 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Isolation, characterization and expression of the A;Reference number: JC4041; MUID:95212917; PMID:7698655
                                                                                                                                                                                                                                                                        R;Nelson, K.E.; Clayton, R.A.; Gill, Garrett, M.M.; Stewart, A.M.; Cotton,
                                                                                                                                                                                                                                                                                                                 oxidoreductase, short chain dehydrogenase/reductase family - Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: A72395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P50166;
A;Accession: PC4017
A; Gene: TM0297
C; Superfamily:
                                                             A;Cross-references: UNIPROT:Q9WYD3; A;Experimental source: strain MSB8
                                                                                                                                                                 A; Reference number: A72200; A; Accession: A72395
                                                                                                                                                                                                                                   Nature 399, 323-329, 1999
                                                                                                      A; Residues: 1-257 < ARN>
                                                                                                                        A; Molecule type: DNA
                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                             A; Title: Evidence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Superfamily: ribitol dehydrogenase; short-chain alcohol de;Keywords: NAD; oxidoreductase;Z1-216/Domain: short-chain alcohol dehydrogenase homology;21-51/Region: beta-alpha-beta NAD nucleotide-binding fold;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                           Genetics
                          TM0297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 NAEKMYKYNLLGSLYVSQAFAKPLIKEGIKGASVYLIGSMSGAIVNDFQNQVYYNMSKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149;
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  ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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                                                                                                                                                                                         lateral gene transfer between Archaea 72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                        R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.3%;
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Pred. No. 1.5e-55;
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                                                                                   GB:AE001711; GB:AE000512; NID:g4980788; PIDN:AAD353
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                                                                                                                                                                                                               126 MVKVNILGSLYVS----QAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAG 181
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                                           YIGAVLYLLSESAASYTTGASLLVDGGFT
                                                                                                                 VIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPKE
                                                                                                                                                                          VVDVDLKGVGYVAKHAGRHFRERFEKEGKKGA-LVFTASMSGHIVNVPQFQATYNAAKAG
                                                                                                                                                                                                                                                                                                  EVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAG--YCENFPCEDYPAKNAEK 125
                                                                                                                                                                                                                                                                                                                                              FKLNGKVASITGSSSGIGYALAEAFAQVGADVAIWYNSHDATGKAEALAKKYGV-----
                                                                                                                                                                                                                                                                                                                                                                                     FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK
                                                                                       VRHFAKSLAVEFAPF-ARVNSVSPGYINTEISDFV---PQETQNKWWSLVPLGRGGETAE
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> 241 197

253

138

82

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carbonyl reductase (NADPH2) (EC 1.1.1.184) - Candida magnoliae
N;Alternate names: aldehyde reductase 1; NADPH-dependent carbonyl reductase
C;Species: Candida magnoliae
                                                                             A;Molecule type: protein
A;Residues: 2-25;79-83;107-124;125-134;149-152;169-189;204-228 <YA2>
C;Genetics:
A;Gene: S1
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
C;Keywords: carbohydrate metabolism; oxidoreductase
                                                                                                                                                                                                    A,Cross-references: UNIPROT:Q9C4B3
A,Experimental source: strain AKU4
A,Accession: PC7090
                                                                                                                                                                                                                                                                                                         Biosci. Biotechnol. Biochem. A, Title: Molecular cloning ar A, Reference number: JC7338 A, Accession: JC7338
                                                                                                                                                                                                                                                                                                                                                                   R;Yasohara, Y.; Kizaki, N.; Hasegawa, J.; Wada, M.; Kataoka, M.;
Biosci. Biotechnol. Biochem. 64, 1430-1436, 2000
                                                                                                                                                                                                                                                                  A; Residues: 1-283 < YAS>
                                                                                                                                                                                                                                                                                 A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                             Date: 08-Sep-2000 #sequence_revision; Accession: JC7338; PC7090
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                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSLKRKVALVTGGGQGIGKAIAQALAAAGAAVLIMDINEE-TARRTVE----
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Conservative
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                   26.7%;
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48;
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                   Score 378; DB 2;
Pred. No. 1.9e-22;
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  Mismatches 100;
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                                      Length 283;
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RESULT 6
B97588
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A; Residues: 1-262 < KUR>
A; Cross references: UNIPROT: Q8UE64; GB: AE007869; PIDN: AAK87659.1;
                                             A; Map position: circular chromosome C; Superfamily: ribitol dehydrogenase;
                                                                                                                                                                                                                                                                                                                   A;Title: Genome Sequence of A;Reference number: A97359; A;Accession: B97588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oxidoreductase, short chain dehydrogenase/reductase family [imported] - Agrobacterium C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004 C;Accession: B97588
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A; Map posi
                                                                                                                    A;Gene: AGR_C_3482
                                                                                                                                                                                                                                                                                                                                                                                                                         Science 294, 2323-2328, 2001
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung,
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                                                                                                                                                                                                                                                                                      A;Status: preliminary
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A;Residues: 1-262 <KUR>
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;Experimental source: strain C58 (I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMAMEWVGRGIRVNTISPGYTATPM----NTRPEMVHQTKLFEEQTPMQRMAGVDEMVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DINIKGVFLSCQABANAMLKNG-RGA-IVNIASMSGVIVNRGLMQCHYNASKAGVIHMSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAGVIHLAK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVLYLLSESAASYTTGASLLVDGGFTSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLACEWAKYNIRVNSLNPGYIYGPLTKUVINGNEELYNR---WISGIPQQRMSEPKEYIG
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                                                                                                                                                                                                                                                                                                                                                  the Plant Pathogen and Biotechnology MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Mismatches 109;
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                                                 short-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miller, N.; Blanchard, M.; Qurollo, Doughty, D.; Scott, C.; Lappas, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.; Krespan,
                                             alcohol dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                      Agent Agrobacterium tun
                                                                                                                                                                                PID:g15157014;
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Markelz,
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kelz, B.
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RESULT 8
F69400
2-deoxy-D-gluconate 3-dehydrogenase (kduD) homolog -
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A;Experimental source: strain 972h-; C;Genetics:
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sorbitol utilization protein soul - fission yeast (Schizosaccharomyces pomb C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: SPDB: SPAC8E11.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-255 < MCL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: Z21831
A;Accession: T39164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;McLean, J.; Harris, D.; Wood, V.; submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: T39164
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Best Local S
Matches 96
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                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                         172
   228
                                                                                                         184
                                                                                                                                                                              125 -KMVKVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAGVI 183
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                                                                                                                                                                                                                   57 HGVQAKAYSCPIENRSAVIETTNQAVEELGGRLDVMIANAGIAIPHLSLED----KNEDIW 113
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                                                                                                       HLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPKEYI 243
                                                                                                                                          TKVVGINLNGAYYTAQAAGHHFKKQG-KG-SLIFTASMSGHIANWPQQWASYHATKAAVK 171
                                   GAVLYLLSESAASYTTGASLLVDGGFTS
                                                                       HLARALAVEWAPF-ARVNSVSPGYIDTDLT---LYADENLRKKWKEYTPQARIGLPDELP
                                                                                                                                                                                                                                                   EVPKMGSYACDISDSDTVHKVFAQVAKDF-GKLPLHLVNTAGYCENFPCEDYPAKNAE-- 124
GAYLYLASD-ASSYCTGSDIIVDGGYCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAIFLLSD-AASFVTGVDLLVDGGFCCW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVPKWGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAGYCENFPCEDYPAKNAEKWV
                                                                                                                                                                                                                                                                                         FSLKGKTTLITGGSGGIGFSIAKAFAAAGSNVGLL-YGRNKKALEYA--
                                                                                                                                                                                                                                                                                                                           FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---KSIQIAADVTSKQALTDAVARTQAELGALSL-AVNAAGIANANPAEEMEESQFQTMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK 67
                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                             25.5%;
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                                                                                                                                                                                                                                                                                                                                                                             Score 361; DB 2;
Pred. No. 3.7e-21;
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Pred. No. 2.5e-22;
3; Mismatches 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL:AL021817; cosmid c8E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barrell, B.G.;
February 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                              Mismatches 103;
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                                   271
 254
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                                                                                                                                                                                                                                                                                                                                                                                              Length 255
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                                                                                                                                                                                                                                                                                         ---- AELRDK 56
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Archaeoglobus fulgidus

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Fleischmann, R.D.; Quackenbush, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, A;Authors: The complete genome sequence of the hyperthermophilic, sulfate-reducing archa A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Atcession: F69400
A;Stating, N.S.; PMID:9389475
A;Atcession: F69400
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F69400
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable short chain oxidoreductase YPO1287 [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Cacession: AC0157
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
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A; Residues: 1-281 <KLE>
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                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: AB0001; A; Accession: AC0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                 A; Cross-references:
                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-271 < KUR>
                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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Best Local S
Matches 91
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Best Local S
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        GHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAK----QAEYHKYATEELKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDLIGAVVFFASD-ASNFVTGQILYIDGGVTSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYIGAVLYLLSESAASYTTGASLLVDGGFTSW 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAVNMITKQLACEWAKYNILVNAIAPTVIATPLTAHIMK-DPELSKTMKSRILLGRWGYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGVIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNBELYNRWISGIPQQRMSEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKNAEKMVKVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSK 179
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                                                                                                                                                                                                                              ribitol dehydrogenase; short-chain alcohol dehydrogenase
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                                                                                                                                                                                                                                                                                                                 UNIPROT: Q8ZGK4; GB:AL590842; PIDN: CAC90118.1; PID: g15979338; GSPDB
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                                                                                                                                           24.7%; Score 349; DB 2; 34.3%; Pred. No. 3.5e-20;
                                                                                                                                                                        Length 271
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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: D72377
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C;Accession: D70635
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc; Connor, R.; Davies, R.; Devlin, K.; Seeger, K.; Skelton, S.; Squares, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Autthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Autthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Rv1928c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul_1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
F;12-194/Domain: short-chain alcohol dehydrogenase homology <SADH>
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A;Experimental source: strain H37Rv
C;Genetics:
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Best Local
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                       GAVLYLLSESAASYTTGASLLVDGGFT
                                                                                                                     HLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPKEYI 243
                                                                                                                                                                                                       EKMVKVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAGVI 183
GLYLYLASE-ASSYMTGSDIVIDGGYT
                                                                                         HLTKAMAVELAPHKIRVNSVSPGYI---LTE-LVEPYTEYQPLWEPKIPLGRLGRPEELA
                                                                                                                                                                                QRLQNTNVTGVFLTAQAAAKAMVKQG-QGGVIINTASMSGHIINVPQQVSHYCASKAAVI
                                                                                                                                                                                                                                                                      EIGTSGGKVVPVCCDVSQHQQVTSMLDQVTAELGGIDIAVCN-AGIITVTPMLDMPLEEF 112
                                                                                                                                                                                                                                                                                                                   EVPKNGS----YACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAGYCENFPCEDYPAKNA 123
                                                                                                                                                                                                                                                                                                                                                                                                            FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK
                                                                                                                                                                                                                                                                                                                                                                  FDLHGKRALITGASTGIGKRVALAYVEAGAQVAI-----AARHLDALEKL-AD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 344; DB 2; Length 255; pred. No. 8.1e-20; 45; Mismatches 108; Indels
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oxidoreductase, short chain dehydrogenase/reductase C_i Species: Thermotoga maritima

family - Thermotoga maritima

(strain

Gill,

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Gwinn,

м. L.;

Dodson,

R.J.;

Haft,

D.H.;

Hickey

D72377 RESULT 11

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A;Title: Complete genome se
A;Reference number: A82950;
A;Accession: D83416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable short-chain dehydrogenase PA1828 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
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A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-255 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q9WYS2; A;Experimental source: strain MSB8
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A; Residues: 1-255 < ARN>
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A;Accession: D72377
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C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Pseudomonas aeruginosa;Date: 15-Sep-2000 #text_change;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change;Accession: D83416
                                                                                                                                                                    Query Match
Best Local !
                                                                                                                                                                                                                             ;Superfamily:
                                                                                                                                                                                                                                              Gene: PA1828
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                                                                                                                                                                      Local Similarity
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Similarity 33.5%;
     EGGKATAIACHIGEMEQIQNVFAQIREQFGRLDI-LVNNAATNPQFC-NVLETDLGA--F
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                                       EVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAG----YCENFPCEDYPAKNA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVFLASEE-AKYVTGQIIFVDGGWTA 254
                                                                                                               FRFDGHLTIVTGACGGLABALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKALAKEWGRYGIRVNVIAPGWYRTKMTEAVFSDPEKL-DYMLKRIPLGRTGVPEDLKGV
                                                                           FDLDGKIAFVSGASRGIGEAIAKLLAQQGAHVI---VSSRKIDGCQ-----AVADAITA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLYLLSESAASYTTGASLLVDGGFTS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPKEYIGA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEVNÍFGTYÝVCREAFS--LLRES-DNPSIINIGSLTVEEVTMP-NISAYAASKGGVASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AFRCDVSNYEEVKKLLEAVKEKFGKLDT-VVNAAGINRRHPABEFPLDEFRQV
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                                                                                                                                                                                                                        ribitol dehydrogenase; short-chain alcohol dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                       sequence of Pseudomonas aeruginosa 50; MUID:20437337; PMID:10984043
                                                                                                                                                                    22.8%; Score 322.5; DB 2; 34.7%; Pred. No. 4.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erwin, A.L.; Mizoguchi, S.D.; Warrener, L.L.; Coulter, S.N.; Folger, K.R.; Kas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cotton,
                                                                                                                                                     48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49; Mismatches 110;
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Pred. No. 3.5e-19;
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                                                                                                                                                   104;
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Larbig,
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C;Accession: T15987

R;Geisel, C.; Gattung, S.
submitted to the EMBL Data Library, November A;Description: The sequence of C. elegans cos A;Reference number: Z18443

A;Accession: T15987
                                                                                                      hypothetical protein F09E10.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #te
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RESULT 13
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A;Residues: 2-26 <8U2>
C;Comment: This enzyme is an NADH-dependent enzyme and belongs to the short-chain
ylitol from D-xylulose or D-arabitol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 22-Jun-2003 #sequence_revision 22-Jun-2003 #text_change C;Accession: JC7939; PC7223
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C;Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references:
A;Accession: PC7223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-262 <SUG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Sugiyama, M.; Suzuki, S.; Tonouchi, N.; Yokozeki, K. Biosci. Biotechnol. Biochem. 67, 584-591, 2003 A;Tille: Cloning of the xylitol dehydrogenase gene from A;Reference number: JC7939; MUID:22608835; PMID:12723607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xylitol dehydrogenase (EC 1.1.1.-) - Gluconobacter oxydans (Strain C;Species: Gluconobacter oxydans (Strain ATCC621)
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Best Local :
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                                                                                170
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  227
                                       232
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                                                                                                                                                                                                                                    58 ---ARSYVCDVTSEEAVIGTVDSVVRDFGKIDF-LFNNAGYQGAFAPVQDYPSDDFARVL 113
                                                                                                                                                                                                                                                                         69 VPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAGYCENF-PCEDYPAKNAEKMV 127
                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                    NADH-dependent enzyme; short-chain dehydrogenase/reductase
                                                                                                                                                                                                                                                                                                                                                                                                  86;
                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                    PQQRMSEPKEYIGAVLYLLSESAASYTTGASLLVDGG 268
                                                                                                                                                          TINVTGAFHVLKAVSRQMITQNY--GRIVNTASMAG--VKGPPNMAAYGTSKGAIIALTE 169
PMRRYGDINEIPGVVAFLLGDD-SSFMTGVNLPIAGG
                                                                         TAALDLAPYNIRVNAISPGYM-GPGFMWERQVELQAKV--GSQYFSTDPKVVAQQMIGSV
                                                                                                                 TLACEWAKYNIRVNSLNPGYIYGP-----LTKNVINGNE------ELYNRWISGI 231
                                                                                                                                                                                                                                                                                                                  KFNGKVCLVTGAGGNIGLATALRLAEEGTAIALLDMNREALEKAEASVREKGVE-----
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                                                                                                                                                                                                                                                                                                                                                                                                              22.7%; Score 321.5; DB 2; 31.0%; Pred. No. 5e-18;
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-255 <GEI>
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A;Introns: 5/2; 101/3; 126/3; 184/3
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein alr4456 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence revision 14-Dec-2001 #text_change 09-Jul-2004 C;Date: 14-Dec-2001 #sequence revision 14-Dec-2001 #text_change 09-Jul-2004 C;Accession: AH2362
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A;Gene: CESP:F09E10.3
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A;Experimental source: strain Bristol N2; clone F09E10
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C;Superfamily:
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183
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131
                                             132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 YACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAGYCENFPCEDYPAKNAEKMVKVNLLGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 SGGASGIGKAISQTLAKHGARVVVADLDSGNAAA-----TAKALPASQSHSS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 TGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLKEVP---KMGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 PACDVSNADSV-KGLSEHVKSLG-TPSILVNCAGITKDSTLLKMKQEQWDSVIKVNLTGV 124
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TSIFELSRLF-YPLLKTS-KNSSIVNIGSVAGLI--SVRTGAPYGMTKAALVQLTRSLAV
                                          LGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAGVIHLAKTLAC 191
                                                                                                                                          MGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAGYCENFPCEDYPAKNAEKMVKVNL 131
                                                                                                                                                                                          GRKALITGATKGIGLAIAQEFLALGAEVVIVARNAEAIEQQMKAWH------SAGK 71
                                                                                                                                                                                                                   GHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLKEVPK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSYVIGATLEVIGGES 254
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                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                21.6%; Score 305.5; DB 2; 30.7%; Pred. No. 9.5e-17;
                                                                                                                                                                                                                                                                                            Mismatches 109;
                                                                                                                                                                                                                                                                                                                                    Length 267;
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                                                                                                                                                                                                                                                                                            Gaps
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Search completed: July 9, 2005, 10:31:43 Job time: 42 secs

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Scoring table:
                                                                                            Sequence:
                                                                                                                  Perfect score:
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                                                                                                                                                                                                                                                   protein search, using sw model
                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                  US-10-720-018-2
1415
1612378 seqs, 512079187 residues
                                                                                              1 MTDYIPTFRFDGHLTIVTGA.....SAASYTTGASLLVDGGFTSW 272
                                                                                                                                                                         July 9, 2005, 10:19:36 ; Search time 178 Seconds
(without alignments)
782.503 Million cell updates/sec
                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

1612378

RESULT 1

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Database UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 798.5 797.7 769.5 5669.5 528.5 510.5 Score 100.0 56.4 56.3 54.3 47.3 37.3 Query Match Length DB QEBNIE DCXA TRIRE OB9QA5 Q7RZD4 Q6BQ25 SOUL CANAL O9ZMP6 Q9C4B3 Q9C4B3 Q70FD1 ARDH_CANAL ARDH_PICST ARDH_CANTR Q8UE64 Q6CM06 S0U2 Q Q9Y6Z9 Q9Y6Z9 Q86ZP3 Q86ZP3 Q86ZP3 Q86ZP3 Q86ZP3 Q6BY61 Q6CX46 Q6C367 Q6T5L8 Q7SE47 Q6C6W8 Q6SSP1 Q6SSP1 Q9WYD3 CANAL Q70fd1 ambrosiozym p43066 candida alb p50167 candida tro Q6by61 debaryomyce Q6cx46 kluyveromyce Q6cx46 kluyveromyce Q6cx46 kluyveromyce Q6c587 yarrowia li Q6t518 emericella Q7se47 neurospora Q6c6w8 yarrowia li Q65sp1 mannheimia Q9wyd3 thermotoga Q6bn16 debaryomyce Q8nk50 trichoderma Q89q45 bradyrhizob Q7rzd4 neurospora Q6bq25 debaryomyce P87219 candida alb Q9amp6 rhizobium m Q9c4b3 candida mag Q92mr6 rhizobium m Q9c4b3 candida alb Q9zmc6 rhizobium m Q9c4b3 candida alb Q9zmc6 rhizobium m Q8ue64 agrobacceri Q6cm06 kluyveromyc P87218 candida alb Q9ybz9 schizosacch Q8szp3 gibberella Q7sch3 neurospora Q7sch3 neurosporiu Q9sch3 candida pseudomonas Q66cct3 yersinia ps Description

| 354.5 25.1 266 2 QBJZ31 QBJZ31 350 24.7 271 2 QSZGK4 QBZZK4 QBZZK5 QZZZK5 QBZZK5 QBZZK | 45 |
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| 266 2 QBJZ31 271 2 QSZCK4 271 2 QSZCK4 257 2 QBZCK5 269 2 QBBZCS 269 2 QGBKS 273 2 QSBHS 273 2 QSHS 275 2 QFTZ97 255 2 PFSJS6 255 2 QFTZ97 268 2 QFTZ97 268 2 QFTZ97 278 2 QGCEE9 285 2 QFGCEE9 | 339 |
| 2 Q8JZ31 2 Q7SZ74 2 Q8ZGK4 2 Q8CQE7 2 Q8FQE5 2 Q8FQE5 2 Q6BNC5 2 Q9HJ4 2 P95286 2 Q7JZ27 3 Q6BQZ8 | 24.0 |
| | 285 |
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| Q8J231 Q782t4 Q8zgk4 Q8zgk7 Q8fz65 Q6bn65 Q92m73 Q99h)4 P95286 Q7tz97 Q986J1 Q73zf4 Q6cee9 Q6cee9 | Q6BQ28 |
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| alternaria neurospora yersinia pe staphylococ brucella su debaryomyce rhizobium m bradyrhizob mycobacteri mycobacteri rhizobium 1 mycobacteri yarrowia li debaryomyce | |

ALIGNMENTS

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| 181 GVIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPK 240 | 181 GVIHLAKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPK 240 | 121 KNAEKWYKVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKA 180 | 121 KNAEKWYKVNILGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDEQNQVVYNMSKA 180 | 61 TEELKLKEVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAGYCENFPCEDYPA 120 | 61 TEELKLKEVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAGYCENFPCEDYPA 120 | 1 MTDY1PTFRFDGHLT1VTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYA 60 | 1 MTDYIPTFRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYA 60 | Query Match 100.0%; Score 1415; DB 2; Length 272; Best Local Similarity 100.0%; Pred. No. 7.3e-107; Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | NON TER 272 272 | PROODER; GDHRDH. | S; PRO1415; ANKYRIN. | InterPro; IPRO02110; ANK. | IPR002347; | GO; GO:0000133; r:WeddD0115W; 15A. InterPro; IPR002198; ADH short. | F:oxidoreduct | P; P50162; 1AE1. | C. BLUI. CIEH. 4/9:14/30-14/31/2004/. EMBI: AUSB3159: CAB47547.1: - | pathway of yeast."; T Biol Chem 270:14746-14751(2004) | in the L-arabinose co | Verho R. Dutkonen M. Iondeshorough J. Denttilae M. Richard D. | STRAIN=NRRL Y-1484; DibMod-14736891. DOT-10 1074/355 M313533300. | SEQUENCE FROM N.A. | [1] | Saccharomycetales. Saccharomycopsidaceae; Ambrosiozyma. NCBT TavTD-47089. | | Ambrosiozyma monospora. | Namesalx1: | Last annotation | (TrEMBLrel. 27, Last sequence up | Q/OFUL; 05-JUL-2004 (TrEMBLrel. 27, Created) | Q70FD1 PRELIMINARY; PRT; 272 AA. | ₽ |

241

EYIGAVLYLLSESAASYTTGASLLVDGGFTSW

272

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ARBSULT 2
ARDH CANAL
ID ARDH C
ARDH C
ARDH C
ARDH C
ARDH C
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DR CANAL
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Best Local S
Matches 151
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94012494; PubMed=8407803;
Wong B., Murray J.S., Castellanos M., Croen K.D.;
"D-arabitol metabolism in Candida albicans: studies of the
biosynthetic pathway and the gene that encodes NAD-dependen
arabitol dehydrogenase.";
J. Bacteriol. 175:6314-6320(1993).
J. Bacteriol. 175:6314-6320(1993).
-I- CATALYTIC ACTIVITY: D-arabinitol + NAD(+) = D-ribulose
-I- PATHWAY: D-arabinitol biosynthesis; last step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=ARD1; Synonyms=ARDH; Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002198; ADH_short.
InterPro; IPR002347; Adh_short_C2.
Pfam; PF00106; adh_short; 1.
PRINTS; PR00081; GDHRDH.
PRINTS; PR00080; SDRFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L16227;
HSSP; Q9ZFY9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=WO-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycetales; mitosporic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGR01830; 30xo_ACP_reduc; TIGRFAMS; TIGR01831; fabG_rel; 1. TIGRPAMS; TIGR01832; kduD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SITE
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                                                                                                                                                                                                                                                                                                                           Similarity
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                         NAEKAVKVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKAG
                                                                                                                            KLK---EVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAGYCENFPCEDYPAK
                                                                                                                                                                                               VPSFRLDGKLVILTGGSGGLAAVVSRALLAKGADVALVDMNLERTQQAARDVLQWGEEQM
                                                                                                                                                                                                                              IPTFRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEEL
                                                                                               KGKYESPIGQVSAWSCNIGDAEAVDLTFKAINEHHGKISSVLVNTAGYAENFPAEEYPAK
  NAENLMKVNGLGSFYVSQAFARPLIQNNMTG-SIILIGSMSGTIVNDPQPQCMYNMSKAG
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281
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(Rel. 45, Last annotation update)
2-dehydrogenase [ribulose forming]
                                                                                                                                                                                                                                                                                                    Conservative
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1FK8.
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184
169
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                                                                                                                                                                                                                                                                                                    55;
                                                                                                                                                                                                                                                                                                                                                                                                 NAD (By similarity).
Proton acceptor (By similarity).
Substrate (By similarity).
; B302A6411691F892 CRC64;
                                                                                                                                                                                                                                                                                                                        Score 800; DB 1;
Pred. No. 8e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
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                                                                                                                                                                                                                                                                                                                                                  281;
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Matches 151
                                                                                                                                                              InterPro; IPR002198; ADH_short.
InterPro; IPR002347; Adh_short_C2.
Pfam; PF00106; adh_short; 1.
PRINTS; PR00081; GDHRDH.
PRINTS; PR00080; SDRFAMILY.
TIGRFAMS; TIGR01830; 30x0 AcP_reduc; 1.
TIGRFAMS; TIGR01831; fabG_rel; 1.
TIGRFAMS; TIGR01831; kduD; 1.
PROSITE; PS00061; ADH_SHORT; 1.
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25-OCT-2004 (
D-arabinitol
                                                                                                               NAD; Oxid
NP BIND
ACT SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-ATCC 58785 / CBS 6054;
MEDLINE=96090133; PubMed=7483848;
Hallborn J., Walfridsson M., Pent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pichia stipitis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A short-chain dehydrogenase gene from Pichia stipitis arabinitol dehydrogenase activity."; Yeast 11:839-847(1995).
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                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents
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 DYSYANVVPNFRLDGRLAIITGGSGGLAAVISRALLAQGADVALIDMNLERTKSAAKEVL
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(Rel. 45, Last annotation update)
2-dehydrogenase [ribulose forming]
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                                                 Score 798.5; DB
Pred. No. 1e-56;
4; Mismatches
                                                                                                   Proton acceptor (By similarity).
Substrate (By similarity).
; 36869165F23964F6 CRC64;
                                                                                                                                          NAD (By similarity).
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MEDLINE-94071892; PubMed=8250887;

Quong M.W., Miyada C.G., Switchenko A.C., Goodman T.C.;

Quong M.W., Miyada C.G., Switchenko A.C., Goodman T.C.;

"Identification, purification, and characterization of a D-arabinitol

"Identification, purification, and characterization, and characterization, and characterization, and ch
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                                                                                                      TIGRRAMS; TIGRO1830; 30x0 ACP_reduc;
TIGRAMS; TIGRO1831; fabG_rel; 1.
TIGRRAMS; TIGRO1832; kdub; 1.
PROSITE; PS00061; ADH SHORT; 1.
DIrect protein sequencing; NAD; Oxide
                                                                                                                                                                                                                                                                                                           InterPro; IPR002198; ADH short.
InterPro; IPR002347; Adh short_C2.
Pfam; PF00106; adh short; 1.
PRINTS; PR00081; GDHRDH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; JC4041; JC4041.
HSSP; Q9ZFY9; 1FK8.
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(Rel. 34, Last sequence update)
(Rel. 45, Last annotation update)
[ 2-dehydrogenase [ribulose forming]
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NAD (By similarity).
Proton acceptor (By similarity).
Substrate (By similarity).
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A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
B Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potter S., Richard G.F., Straub M.L., Suleau A.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Wincker P., Souciet J.L.,
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Q6BY61;
25-OCT-2004 (TrEMBLrel. 2
25-OCT-2004 (TrEMBLrel. 2
25-OCT-2004 (TrEMBLrel. 2
                                                                                                Genoscope;
Submitted
(SDR) family.

EMBL; CR3.82113; CAG84833.1; -.

GO; GO:0016491; F:oxidoreductase activity;

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR002199; ADH short.

InterPro; IPR002347; Adh_short_C2.
                                                                                                                                                         Nature 430:35-44(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORFNames=DEHA0A12595g;
Debaryomyces hansenii CBS767.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                                                                                                            SEQUENCE FROM N.A. STRAIN=CBS767;
                                                                                                                                                                                                                                                                                                                                                                                               Genolevures;
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SIMILARITY: Belor
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babbur A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Hantraye F., Hemnequin C., Jauniaux N., Joyet P., Kachouri R.,
A Hantraye F., Hemnequin C., Jauniaux N., Joyet P., Kachouri R.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
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A Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
A Pellenz S., Potier S., Wesolowski-Louvel M., Westhof E., Wirth B.,
A Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
A Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Wincker P., Souclet J.L.;

M. Wincker P., Souclet J.L.;
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Q6CX46;
25-OCT-2004
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PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH-SHORT; UNKNOWN
Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kluyveromyces lactis NRRL Y-1140.
Eukaryota; Fungi; Ascomycota; Saccharom
Saccharomycetales; Saccharomycetaceae;
NCBI_TaxID=284590;
Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382121; CAH03081.1; -.
GO; GO:0016491; F:oxidoreductase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=NRRL Y-1140;
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ORFNames=KLLA0A11352g;
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                                                                                                              STRAIN=NRRL
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                                                                                                                                                                                                                         "Genome evolution in yeasts.";
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'S; PR00081; GDHRDH.
'S; PR00080; SDRFAMILY.
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Y-1140;
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stipitis D-arabinitol 2
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cetaceae; Kluyveromyces
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                                                                                        RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Faithead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellerz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Wincker P., Souciet J.L.;
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
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25-OCT-2004
25-OCT-2004
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PROSITE; PS00061; ADH SHORT; UNKNOWN
SEQUENCE 314 AA; 34138 MW; 615ED
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InterPro; IPR002347; Adh_sho
Pfam; PP00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   lipolytica.
lipolytica.
ORFNames=YALIOF02211g;
ORFNames=YALIOF02211g;
Genoscope;
Submitted (JUL-2004)
-!- SIMILARITY: Belor
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Eukaryota; Pungi; Ascomycota; Saccharomycotina;
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25-OCT-2004 (TrEMBLrel. 28, Las
25-OCT-2004 (TrEMBLrel. 28, Las
25-OCT-2004 (TrEMBLrel. 28, Las
Yarrowia lipolytica chromosome
                                        SEQUENCE FROM |
STRAIN=CLIB99;
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                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                  430:35-44(2004).
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Adh_short_C2.
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the short-chain dehydrogenas
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Pred. No. 3.
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Best Local :
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GO; GO:0016491; F:oxidoreductase activity; IE
GO; GO:0018152; P:metabolism; IEA.
InterPro; IPR002198; ADH_short.
InterPro; IPR002347; Adh_short_C2.
InterPro; IPR0002347; Adh_short_C2.
InterPro; IPR000205; NAD_BS.
Pfam; PF00106; adh_short; 1.
PRINTS; PR00016; ADH_SHORT; UNKNOWN_1.
PRINTS; PR00080; SDRPAMILY.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                05-JUL-2004 (
05-JUL-2004 (
05-JUL-2004 (
D-arabinitol
J. Biol. Chem. 279:4578-4587(2004).
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/red (SDR) family.
EMBL; AY434691; AAR85467.1; -.
EMBL; AY387591; AAR23109.1; -.
GO; GO:0047038; F:D-arabinitol 2-dehydrogenase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
                                                                                                                                                                                  SEQUENCE FROM N.A.

Rodriguez J.M., Ruiz-Sala P., Ugarte M., Penalva M.A.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                               SEQUENCE FROM N.A.

PubMed=14612443; DOI=10.1074/jbc.M310055200;

Pobmed=14612443; DOI=10.1074/jbc.M310055200;

Rodriguez J.M., Ruiz-Sala P., Ugarte M., Penalva M.A.;

"Fungal Metabolic Model for 3-Methylcrotonyl-CoA Carboxylase"
                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycot:
Eurotiales; Trichocomaceae;
EURI TaxID=162425;
                                                                                                                                                                                                                                                                   Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
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SEQUENCE 343 AA; 37082 MW;
                                                                                                     Deficiency."
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L; CR382132;
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                                                                                                                                                                                                                                                                                                               Created)
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Last annotation updat
(EC 1.1.1.250).
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Pred. No. 1.3e-34;
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Best Local S
Matches 106
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InterPro; IPR002198; ADH short.
InterPro; IPR002347; Adh_short_C2.
Pfam; PP00106; adh short; 1.
PRINTS; PR00081; GDHRDH.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
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01-MAR-2004 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pe
Sordariomycetidae; Sordariales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=NCU02128.1
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01-MAR-2004
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                                                                          (SDR) family.
                                                                                                                                                          Nature 0:0-0(2003)
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                                                  EMBL/GenBank/DDBJ
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50; Mismatches
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s; Sordariaceae;
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                                                                                      Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Despons L., Fabre E., Fairhead C., Ferry Dumazet H., Groppi A.,
A Despons L., Fabre E., Lemaire M., Lesur I., Ma L., Muller H.,
A Merrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Oztae-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
B Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
A Bincher D. Conciet T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P42556; 1P33.
GO; GO:0016491; F:oxidoreductase activity; IE
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR002198; ADH_short.
InterPro; IPR002347; Adh_short; C2.
IPR00106; Adh_short; 1.
PRINTS; PR000081; GDHRDH.
PRINTS; PR00081; GDHRDH.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
HYPOTHELICAL PROTEIN; Oxidoreductase.
SEQUENCE 371 AA; 39631 MW; 4BC6D601508DFE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to tr[O9MYD3 Thermotoga maritima TM0297 Oxidoreductase.
ORFNames=YALI0E05643g;
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25-OCT-2004 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=284591;
                                                                                                                                                                                                                                                                                                                                                                                                                       Yarrowia lipolytica CLIB99.
                                                                                                                                                                                                                                                                                                            GenoLevures;
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                  SEQUENCE FROM N.A.
                                                Nature 430:35-44(2004)
                                                                                 Wincker P.,
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                                                               evolution in yeasts.";
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                                                                                Souciet J.L.;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.4e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetes;
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                                                                                                    Weissenbach J.
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RESULT 11
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Best Local S
Matches 99
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Best Local Similarity
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InterPro; IPR002347; Adh_short_C2
Pfam; PF00106; adh_short; 1.
PRINTS; PR00081; GDHRDH.
PRINTS; PR00080; SDRFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope;
Submitted (JUL-2004) to
-!- SIMILARITY: Belongs
(SDR) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase. sequence 291 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; CR382131; CAG79175.1; -.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                            Mannheimia succiniciproducens MBEL55E
Bacteria; Proteobacteria; Gammaproteol
Pasteurellaceae; Mannheimia.
                                                                                                                                                                                                                                                                                      Q65SP1;
25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00061; ADH_SHORT; UNKNOWN
                                                                                                                                                      STRAIN=MBEL55E;
Hong S.H., Kim J.S.,
Kim C.H., Jeong H.,
                                                                                                                                                                                                                                                                FabG protein.
Name=fabG; ORFNames=MS1412;
                                                                                                                                                                                                                                                                                                                                       Q65SP1
                                                                                            Nat. Biotechnol. 0:0-0(2004).
EMBL; AE016827; AAU38019.1; -
SEQUENCE 259 AA; 27552 MW;
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                              "The genome sequence
succiniciproducens.";
                                                                                                                                                                                                                NCBI_TaxID=221988;
                                                                                                                                                                                                                                                                                                                                                                                                                        232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLGRLGDPDELTGACIYLASD-ASSYVTGSDIIIDGGYT 289
                                                                                                                                                                                                                                                                                                                                                                                                                          POORMSEPKEYIGAVLYLLSESAASYTTGASLLVDGGFT
                      RFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDID---QEKTAAKQAEYHKYATEELK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSAYNASKAAVKHLSKSLAAEWAVHNIRCNSISPGYMDTALNR----
KLTGKTAFVTGGARGIGKSVAIAFAQAGANVVIADFDIAEAEKTAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAG79175.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31002 MW; 9479873014C4101D CRC64;
                                                                                                                                            , Lee S.Y., In Y.H., Choi
Hur C.-G., Kim J.G.;
e of the capnophilic rumer
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                                                            28.8%;
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                                                                                                                                                                                                                                                                                         228,
28,
                                                                                                                                                                                                                                           Gammaproteobacteria;
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the short-chain dehydrogenases/reductases
                                                44;
                                                                                                                                                                                                                                                                                         Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 465; DB 2;
Pred. No. 1.5e-29;
                                               Score 407; DB 2; Pred. No. 6.7e-25; 4; Mismatches 104;
                                                                                                B46EF478E3F5923C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                       sequence update)
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                                                                                                                                                                      s.s.,
                                                                                                                                               bacterium Mannheimia
                                                                                                                                                                                                                                             Pasteurellales;
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Best Local Similarity
                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MSB8 / DSM 3109 / ATCC 43589;
MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
McDonald L.A., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., White O.,
Stewart A.M., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg J.F., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9WYD3;
Q9WYD3;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE001711; PIR; A72395, A72395.
                                                                                                                                                                                                                              PRINTS; PRO0081; GDHRDH.
PRINTS; PRO0080; SDRFANILY.
PROSTIE; PRO0061; ADH SHORT; UNKNOWN_1.
Complete proteome; Oxidoreductase.
SEQUENCE 257 AA; 27886 MW; 724484FF
                                                                                                                                                                                                                                                                                                       GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR002198; ADH short.
InterPro; IPR002347; Adh short_C2.
Pfam; PF00106; adh short; 1.
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01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2004 (TrEMBLrel. 26,
Oxidoreductase, short chain
                                                                                                                                                                                                                                                                                                                                                                                       TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OrderedLocusNames=TM0297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the short-chain
                                                                                                                                                                                                                                                                                                                                                                       GO:0016491; F:oxidoreductase activity;
                    121
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TM0297; -.
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                                                                                                                                                                      101;
                                                                                                                                                                                                                                                                                                                                                                                                                                   AE001711; AAD35385.1;
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KNAEKMYKVNILIGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVVYNMSKA
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                                              EIKEKĠGEADFYVGDVTKEEDCFGAVKKALDRWGKLDIG-VNNAGIGDWCE---AENYPV 110
                                                                          EVPKMGS----YACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAG---YCENFFCEDYPA 120
                                                                                                        FSLKRKVALVTGGGQGIGKAIAQALAAAGAAVLIMDINEE-TARRTVE------
                                                                                                                                    FRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEELKLK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKTLACEWAKYNIRVNSLNPGYIYGPLTKNVINGNEELYNRWISGIPQQRMSEPKEYIGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VINVNLNGVFLTAQAAGKLMIEQG-TGGSIINTASMSAHIVNVPQPQCAYNASKAGVIQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKEVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAGYCENFPCEDYPAKNABK
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                                                                                                                                                                      Conservative
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                                                                                                                                                                                     28.4%; Score 402.5; 36.9%; Pred. No. 1.5
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Last annotation update)
dehydrogenase/reductase
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RESULT 13
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Stremb M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Wincher P. Schoff I., Scarpelli C., Gaillardin C., Weissenbach J.,
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InterPro; IPR002347; Adh_short C2
Pfam; PF00106; adh_short; 1.
PRINTS; PR00081; GDHRDH.
PRINTS; PR00080; SDRFAMILY.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation updat
Similar to YALIOB161929 Yarrowia lipolytica.
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                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00061; ADH_SHORT; UNKNOWN Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bouchier C., Caudron B., Scarpe Wincker P., Souciet J.L.; "Genome evolution in yeasts.";
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Debaryomyces hansenii 188767.
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0016491; F:oxidoreductase activity; IEA GO; GO:0008152; F:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=CBS767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 430:35-44(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CBS767;
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; CR382138; CAG88708.1; -.
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                                         65
                                                                                                                                                                                                                                                      Similarity
IDLFNLKGKVAVVTGGGQGIGYAICEAYAQAGAEVAIWDISDTSTVATKLE-----
                                                                                                                                                         I PTFRFDGHLTI VTGACGGLAEALI KGLLAYGSDI ALLDI DQEKTAAKQAEYHKYATEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JUL-2004) to the EMBL/GenBank/DDBJ databases.
ARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                               291 AA;
                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                               31685 MW; 7386F67E7DD8E9BD CRC64;
                                                                                                                                                                                                                                               28.2%;
                                                                                                                                                                                                                         50;
                                                                                                                                                                                                                      Score 399.5; DB 2
Pred. No. 3.2e-24;
0; Mismatches 96
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DCXR_TRIRE
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Query Match
Best Local Similarity
Matches 102; Conser
                                                       NP BIND
ACT SITE
ACT SITE
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penttilae M.;
"The missing link in the fungal L-arabinose catabolic pathway, identification of the L-xylulose reductase gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trichoderma reesei (Hypocrea jecorina).
Bukaryota; Fungi; Ascomycota; Pezizomycotina;
Hypocreomycetidae; Hypocreales; Hypocreaceae;
NCBI TaxID=51453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (Rel. 45,
25-OCT-2004 (Rel. 45,
25-OCT-2004 (Rel. 45,
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                                                                                                                                                        TIGRPAMS; TIGRO1830; 30x0 ACP_reduc; 1.
TIGRPAMS; TIGRO1831; fabG_rel; 1.
TIGRPAMS; TIGRO1832; kduD; 1.
                                                                                                                                                                                                InterPro; IPR002198; ADH_short.
InterPro; IPR002347; Adh_short C2.
Pfam; PF00106; adh_short; 1.
PRINTS; PR00081; GDHROH.
PRINTS; PR00080; SDRFAMILY.
                                                                                                                                                                                                                                                                      EMBL; AF375616; AAM20896.1; -. HSSP; Q9ZFY9; 1FK8.
                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http:\bar{l}/www\_isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 41:6432-6437(2002).
-!- FUNCTION: Catalyzes the NADE
D-xylulose, D-fructose, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Richard P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND ENZYME ACTIVITY.
MEDLINE=22005794; PubMed=12009906; DOI=10.1021/bi025529i;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L-xylulose reductase
                                                                                                                             PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
Carbohydrate metabolism; NADP; Oxidoreductase; Xylose metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                          for L-xylulose.
CATALYTIC ACTIVITY: Xylitol + NADP(+) = L-xylulose +
PATHWAY: L-arabinose pathway; third step.
SIMILARITY: Belongs to the short-chain dehydrogenases
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                                                    159
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174
178
 Conservative
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A
              27.8%;
                                                          28478 MW;
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, Last annotation update)
(EC 1.1.1.10) (XR).
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  51;
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              Score
Pred.
                                                    Proton acceptor (By similar
By similarity.
Substrate (By similarity)
; 1CF56334DA86F109 CRC64;
                                                                                                                  NADP (By similarity)
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  Mismatches
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ort-chain dehydrogenases/reductases
                393; DB 1;
No. 9.6e-24;
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                            Length 266;
                                                                                                     similarity).
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RESULT
Q89QA5
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STRAIN-USDA110;
MEDLINE-22484998; PubMed=12597275;
MEDLINE-22484998; PubMed=12597275;
Manako T., Nakamura Y., Sato S., Minamisawa K., Uchium
Kaneko T., Watanabe A., Idesawa K., Iriguchi M., Kaw
Sasamoto S., Watanabe A., Shimpo S., Tsuruoka H., Wada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q89QA5
Q89QA5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 01-MAR-2004 (TrEMBLrel.
                                                                                                                                                        PROSITE; PS00061; ADH SHORT; UNKNOWN_1.
Complete proteome; Oxidoreductase.
SEQUENCE 257 AA; 27403 MW; A49BE3BE
                                                                                                                                                                                                                                                                                                                                      "Complete genomic sequence of nitrogen-fixing symbiotic Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase.
                                                                                                                                                                                             InterPro; IPR002198; ADH_short.
InterPro; IPR002347; Adh_short C2.
Pfam; PF00106; Adh_short; 1.
PRINTS; PR00081; GDHRDH.
PRINTS; PR00080; SDRFAMILY.
                                                                                                                                                                                                                                                                                    EMBL; AP005946; BAC-
HSSP; Q9ZFY9; 1FJH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bradyrhizobium japonicum.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OrderedLocusNames=blr3225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bradyrhizobiaceae; Bradyrhizobium
                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
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                                                                                                                                                                                                                                                                                                               (SDR) family.
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99; Conser
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LKAKGFDAETAIM-----DVTDTRRVAEVANDLVARHGKVDI-LVNNAGIARSETPAETV
                              LKLK----
                                                                             YIPTFRFDGHLTIVTGACGGLAEALIKGLLAYGSDIALLDIDQEKTAAKQAEYHKYATEE
                                                      YLEKPKLDGKTAFITGGGQGIGLACAEALAEAGARVVIGDRDSKVADSAKA------S
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                             EVPKMGSYACDISDSDTVHKVFAQVAKDFGKLPLHLVNTAGYCEN-FPCEDY 118
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Last sequ
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                                                                                                                     Score 392.5; DE Pred. No. 1e-23;
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| 119 PAKNAEKNVKVNLLGSLYVSQAFAKPLIKEGIKGASVVLIGSMSGAIVNDPQNQVYXNMS 178 :::: : :::: :: : ::: : |
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